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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

on: ular output not generated. Wed Jun 24 17:28:39 1998; MasPar time 3146.28 Seconds 1361.982 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-866-354-1 (1-2568) from US08866354.seq 2525 1 AATCTGGCCTCGGAACACGC......CACTCTTGTACAAAAGAAAA 2568
TTAGACCGGAGCCTTGTGCG......GTGAGAACATGTTTTCTTTT

Scoring table: TABLE default Gap 6

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: Dbase 0; Query 0 457396 segs, 834342348 bases x 2

Nmatch

STD :

Database:

Database:

emb154

1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_vi genbank106
13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat 19:gb_ph 20:gb_pl 21:gb_prl 22:gb_pr2 23:gb_ro 24:gb_st 25:gb_sy 26:gb_un 27:gb_vi

atistics: Mean 12.226; Variance 7.675; scale 1.593

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	80	ID	Description	Pred. No.
-	2285	90.5	2560	22	AF038421	Homo sapiens GPI-linke	0.00e+00
N	2011	79.6	2175	22	HSU95847	Human GDNF receptor al	0.00e+00
ω	1619	64.1	1619	22	AF042080	Homo sapiens glial cel	0.00e+00
4	1571	62.2	1707	22	HSU97144	Homo sapiens RET ligan	0.00e+00
5	1243	49.2	3616	23	RNU97142	Rattus norvegicus RET	0.00e+00
6	1241	49.1	2138	23	RNU59486	Rattus norvegicus GDNF	0.00e+00
7	1223	48.4	2549	23	AF014117	Mus musculus GDNF rece	0.00e+00
8	1069	42.3	1651	23	AF015172	Mus musculus GDNF rece	0.00e+00
9	1061	42.0	1415	23	AB000800	Mouse mRNA for GDNF re	0.00e+00
10	970	38.4	1392	23	RN2072	Rattus norvegicus mRNA	0.00e+00
11	615	24.4	3037	17	GGU90541	Gallus gallus GDNF rec	0.00e+00
12	491	19.4	832	22	HSGFRA1G11	Homo sapiens GPI-linke	2.25e-297
13	488	19.3	777	23	AF012811	Mus musculus GDNF rece	2.39e-295
14	339	13.4	596	22	HSGFRA1G06	Homo sapiens GPI-linke	3.42e-195
15	298	11.8	385	22	HSGFRA1G01	Homo sapiens GPI-linke	7.33e-168

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5' untranslated region Cowpox virus (CPV) 160 Cowpox virus A-type in Homo sapiens sulfonylu	Komma caudata nucleomo Plasmodium falciparum Human DNA sequence fro	Homo sapiens GDNF fami P.falciparum mRNA for Drosophila melanogaste Drosophila melanogaste	lens GPI 14 from 5 from 5 from	Homo sapiens GPI-linke Mus musculus GDNF fami Human gilal cell line-Homo sapiens GDNF fami Homo sapiens RET ligan Rattus norvegicus RET Rattus norvegicus gila Homo sapiens GPI-linke Gallus gallus neurturi Homo sapiens GPI-linke Homo sapiens GPI-linke Sequence 34 from Paten Homo sapiens GPI-linke Sequence 14 from paten Sequence 14 from paten
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ALIGNMENTS

	CDS	gene		source	FEATURES	CORNAL	TITLE	AUTHORS	REFERENCE	JOURNAL	THE	7777	AUTHORS	REFERENCE		ORGANISM	SOURCE	NID	ACCESSION	RESULT 1
/gene="Great" /gene="Great" /note="similar to GDNF Receptor alpha; part of functional /note="similar to gdnF Receptor tyrosine kinase" ligand for RET receptor tyrosine kinase" /codon_start=1 /product="GF1-linked anchor protein" /product="FGF1-linked anchor protein" /db_xref="PID:9292132" /translation="MFLATLYFALPFLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST /translation="MFLATLYFALPFLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST KYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRI	5571954	/map="10q25" <1. >2560	/organism="Homo saptens" /db_xref="taxon:9606" /chromosome="10"		Location/Qualifiers	Adelbert Road, Cleveland, OH 44106-4955, USA	010	Halushka,M., Fox,G.M. and Chakravarti,A.	2 (bases 1 to 2560)		a candidate gene for Hirschsprung disease susceptibility	and Chakravarti, A.	Angrist, M., Jing, S., Bolk, S., Bentley, K., Nallasamy, S.,	1 (bases 1 to 2560)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	Homo sapiens	human .	92921531	AF038421	2560 bp mRNA PRI 10-APR-1998

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BASE COUNT Query Match Best Local Simi Matches 2525; 841 858 781 721 738 661 678 601 618 541 558 481 498 421 438 361 378 301 318 241 258 181 198 121 798 138 61 78 18 μ. CGGACCTGAACCCCTAAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTCG GCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTGGAGGATTCCCCAT GCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAGC TGTTCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGGCCGAAG GCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTCA TGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAGTGCCTGAAGGAGCAGA TGTTCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGGCCGAAG TTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCAA TTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCAA TAAATAAACAAACTGGCTCCTCGCCGCAGCTGGACGCGGTTGAGTCCAGGTTGGGT CGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGAG CGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGAG 137 TGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAGTGCCTGAAGGAGCAGA Similarity 642 Conservative æ YWSMYOSLOGNDLLEDSPYEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKA
CNLDDICKKYRSAYITPCTTSVSNDVCNRRKCHKALRGFEDKYPAKHSYGMLEGSCYRS
IACTERRRQTIVPVGSVEEREKRUCLUADDSGKTNYIGRSRLADFFTNCOPESRSVSS
CLKENYADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNSGNDLEECLKFLNFFKD
MTCLKNAIQAFGMGSDVTVWQPAFPVQTTTATTTTALRYKNKPLGPAGSENEIPTHVL
PPCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSCGLSPLLVL
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611 t 90.5%; Score 2285; DB 22; Pred. No. 0.00e+00; 0; Mismatches ω •• Length Indels 2560; 40; Gaps 917 857 797 737 660 677 540 557 480 497 420 437 377 300 317 240 257 120 60 77 840 780 720 600 617 360 'n

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1 (bases 1 to 2175)

1 (bases 1 to 7175)

1 (shiki,T., Kondoh,K., Ichimiya,S., Nimura,Y., Seki,N. Sakiyama,S., Takahashi,H., Ohnuma,N., Tanabe,M., Fuji
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NAIQAFGNGSDVTVWQPAFPVQTTTATTTTALRVKNKPLGPAGSENEIPTHVLPPCAN
LQAQKLKSNVSGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSCGLSPLLVLVVTAL
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2 (bases 1 to 1619)
Shefelbine, S.E., Khorana, S.,
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1 (bases 1 to 1619)
Shefelbine,S.E., Khorana,S., Schultz,P.N., Huang,E., Hu,Z.J., Fox,G.M., Jing,S., Cote,G.J. and Gagel,R.F. Mutational analysis of the GDNF/RET-GDNFRa signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                          /product="glial cell line-derived neurotrophic factor receptor alpha"
/db_xref="pl0-g2801557"
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/translation="mflatlyfalplllllsaevsggdrldcvkasdoclkeoscst kyrtlrocvacketnestakdecrsavealkokslyncherekrokskncldark ywswyoslogndlledspyrepvnsrlsdlfrvypf1sdyfoqveh1pkgnncldark chlddickyrsaxifpcftsvsndvcnrkchkalroffdkvpakhsyghlecscr wssyvoslogndlffrvcoscr carekpnclhuddsckthloffrvcosperskysstolfrvyjosserskpnclhuddsckthloffrvcosperskyssclkenyaddllectkflnffkdutchkrochloschthlofthligerspysstokenyadslagaksshlftrsnappscglsplitylppcanloacklksnygnthlcisngnyekeglgasshlftrsmaappscglsplivl
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/gene="GFRA1"
/note="found to be alternative
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/chromosome="10"
/map="10~~~
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/note="GPI-linked receptor"
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ACTGCCTCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCCAACTACATAGACT
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RESULT 4
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                                          2 (bases 1 to 1707)
Sanicola,M., Hession,C.A., Worley,D.
Walus,L., Robinson,S., Jaworski,G.,
Pepinsky,R.B. and Cate,R.L.
Direct Submission
                                                                                                                           proteins
Proc. Nat
97322356
Submitted (11-APR-1997) Molecular
Center, Cambridge, MA 02142, USA
Location/Qualifiers
                                                                                                                                                                      1 (bases 1 to 1707)
Sanicola,M., Hession,C.A., Worley,D.S.
Walus,L., Robinson,S., Jaworski,G., W.
Pepinsky,R.B. and Cate,R.L.
Glial cell line-derived neurotrophic activation can be mediated by two differences.
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/db_xref="pid:g2282026"
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/translation="MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
/translation="MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
KYRTLRQCVACKETNFSLASGLEAKOECRSAMEALKQKSLYNCRCKRRCMKKEKNCLRI
YMSMYQSLQGNDLLEDSPYEPVNSRLSDIFRVVPFISVEHIPKGNNCLDAKAGNLDD
ICKKYRSAYITPCTTSYSNDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTE
RRRQTIVPVCSYEEREKPNDLVLLQDSCKTNYICRSRLADFFTNCQPEKEVSKDLKK
YADCLLAYSGLIGTVWTPNYIDSSLSVAPWCDCSNGSNDLEECLKFINFFKDNTCLK
NAIQAFGNGSDVTVWQPAFPVQTTATTTTALRYKNKPLGPAGSENEIPTHVLPPCAN
LQAQKLKSNYSGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSCGLSPLLVLVVTAL
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/dev_stage="embryonic"
/tissue_type="kidney"
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                                 GGAGCTGAGTCGCCGGCGGCGGTGG-CTGCCCAGACCCGGAGTTTCCTCTTTCACTGG
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U97142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi;
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/product="ref | 19and 1"
/product="ref | PID: 92282022"
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/translation="mFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
/translation="mFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
/translation="mFLATLYFALPLLDLLMSAEVSGRSINCCKRGKKKEKKCLRI
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CNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRD
CNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRD
LACTERRROTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFTTKOQPEERSVSN
CLKENYADCLLAYSGLIGTVMTPNYVDSSSLSVAPWCDCSNGGNDLEDCKFLNFFKD
MTCLKNAIQAFGNGSDVTMMQDAPPVQTTTATTTTAFKYKNKPLGPAGSENEIPTTYL
PCANLQAQKLKSNYSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPV
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955 c 921 g
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/note="PI-linked
receptor alpha"
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/dev_stage="embryonic day
/tissue_type="kidney"
1. .3616
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257. .1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/strain="Wistar"
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                                       TGTCTCAAAAATGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCA
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U59486
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Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; N
                                      Submitted (29-MAY-1996) Immunology, Thousand Oaks, CA 91320-1789, USA
                                                           2 (bases 1 to 2138)
FOX.G.M., Jing.S.J., Yu,Y., Holst,P.L.,
Antonio,L., Hu.Z. and Louis,J.-C.
Direct Submission
                                                                                                    GDNF-induced activation of the ret mediated by GDNFR-alpha, a novel re Cell 85 (7), 1113-1124 (1996) 96270513
                                                                                                                                                  1 (bases 1 to 2138)
Jing,S.J., Wen,D., Yu,Y., Holst,P.L., Luo,Y., I
Antonio,L., Hu,Z., Cupples,R., Louis,J.-C., Hu
                                                                                                                                             Fox, G
                                                                                                                                                                                    Murinae;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
                             Location/Qualifiers
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1,S., Altrock,B. an
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GCAGCGAAGGCCTGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGTACATCACC
                                        GCAGCCAAGGCCTGCÁACCTGGACGACACCTGTAAGAAGTACAGGTCGGCCTACATCACC
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CNLDDTCKKYRSAYITECTTSMSNEVCNRKCHKALRQFEDKVPAKHSYGMLECSCRD
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                                                                                    ATGGAGCTTAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGATCTCTGCACGCTGA
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Dey, B.K., Wong, Y.W. and Too, H.P. Cloning of a novel murine isofoneurotrophic factor receptor Neuroreport 9 (1) (1998) In present to 2549)
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vacterragtivpvcsyeerrepvlllodsgktrivicrskladeftnocpesrsvsn
vacterragtivpvcspeerrepvlllodsgktrivicrsuschladeftnocpesrsvsn
clkenyadcllaysgligtvmppynyidsslsvapwcdcsnsgndledclkflnffkd
ntclknaiqaegngsdvmmopappvotttatttafriknkplgpagseneipthvl
ppcanloagkkksnysgsthlclsdndygkdglagasshittksmaappscglsslpv
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/strain="C57"
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/note="glial cell-line derived neurotrophic
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1651)
Dey, B.K., Wong, Y.W. and Too, H.P.
Cloning of a novel murine isoform of the glial cell concurrorphic factor receptor
Neuroreport 9 (1) (1998) In press
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Mus musculus
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                                                                                                                                   Submitted (17-JUL-1997) Biochemistry, National Singapore, 10 Kent Ridge Crescent, Singapore Location/Qualifiers
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Dey, B.K., Wong, Y.W. and Too, H.P.
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/gene="GDNFR-beta"
/note="glial cell-line derived neurotrophic
receptor beta."
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1405; Conser
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larity 86.7%;
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//db_xref-"pin:92624963"
//tanslation="MetaTlyYVLPLLDLIMSAEVSGGDRLDCVKASDQCLKEQSCST
//tanslation="MetaTlyYVLPLLDLIMSAEVSGGDRLDCVKASDQCLKEQSCST
KYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRCKKGMKKEKNCLRI
YWSNYQSLQGNDLLEDSPYEPVNSRLSDIFRAVPFISVEHISKGNLCLDAKKACNLDD
TCKKYRSAY ITPOTTSMSNEVCURKKCHKALRQFFDKVPKHSYSMLFCSCRDVACTE
RRRQTIVPVCSYEERERPWCLNLQDSCKYNYICKSRLADFTNCQPESKSVSNCLKEN
YADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNSGNDLEDCLKFLMFFKNNTCLK
NAIQAFGNGSDVTMMQPAPPVQTTJATTTTAFRIKNKPLGPAGSENEIPTHVLPPCAN
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GDNF receptor alpha.

GDNF receptor alpha.

Mus musculus Dorsal root ganglion Schwann cell cell_line:

to mRNA.

Mus musculus

Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; /
Watabe, K.
Regulation
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Mouse mRN
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CTGCAACCTGGATGACACCTGCAAGAAGTACAGGTCCGCCTACATCACCCCCTGTACCAC
                                     TGTTTTCCAGCAAGTGGAACACATTTCCAAAGGGAACAACTGCCTCGATGCAGCCAAGGC
                                                                                    ATACGAGCCGGTTAACAGCAGGCTGTCAGATATATTCCGGGCAGTCCCCGTTCATATCAGA
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                        TGTTTTTCAGCAAGTGGAGCACATTCCCCAAAGGGAACAACTGCCTGGATGCAGCGAAGGC
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Submitted (30-JAN-1997) to the DDBJ/EMBL/GenBank databases.
Kazuhiko Watabe, Tokyo Metropolitan Institute for Neuroscience,
Kazuhiko Watabe, Wasashidai 2-6, Fuchu, Tokyo 183, Japan
Neuropathology; Musashidai 2-6, Fuchu, Tokyo 183, Japan
(E-mail: kazwtbetmin.ac.jp, Tel:0423-25-3881, Fax:0423-21-8678)
1. 1415
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2 (bases 1 to 141
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llarity 88.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="IMS32"
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Pred. No. 0.00e+00;
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SOURCE ORGANISM NID KEYWORDS

g2564301 GDNFR-alpha/TrnR1-delta Norway rat. Rattus norvegicus

DEFINITION ACCESSION

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Rattus no complete AJ002072

norvegicus cds

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GDNFR-alpha/TrnR1-delta

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                                                                              TCCAAGCTGTGGTCTGAGCCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCTATT
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                                                                                                                      TGAAAAAGAAGGTCTCG----GTGCTTCCAGCCACATAACCACAAAATCAATGGCTGCTCC
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   TATGAGCCGGTTAACAGCAGGTTGTCAGATATATTCCGGGCAGTCCCGTTCATATCAG-T
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                                                                                                                              TATGAACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTCATATCAGAT
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Loases 1 to 1392)
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Submitted (16-OCT-1997) 1
NC7/172, Runny
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Similarity 88.2%;
223; Conservative
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/product="confr-alpha/TrnR1-delta protein"
/db_xref="piD:e1154274"
/db_xref="piD:e1154274"
/db_xref="piD:e254302"
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/KYRILRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRI
KYRILRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRCKCKGMKKEKNCLRI
YMSMYQSLQGNDLLEDSPYEPVNSRLSDIFRAVPEISVEHISKGNUCLDAKKCNLDD
TCKKYRSAYITPCTTSMSNEVCURRKCHKALRQFFDKVPAKHSYGNLCLACTE
RRRQTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKEN
YADCLLAYSGLIGTVMTPNYVDSSSLSVAFWCDCSNSGNDLEDCLKFLNFFKDNTCLK
NAIQAGGGSDVTMMQPAPPVQTTTATTTTAFRVKNKPLGPAGSENEIFTHVLPPCAN
LQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLFVLMLTA
LAALLSVSLAETS"
                                                                             -G--A----A-CACATTTCCAAAGGGAACAACTGCCTGGACGCAGCCAAGGCC
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/strain="Hannover"
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Pred. No. 0.00e+00;
0; Mismatches 145;
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SOURCE ORGANISM

chicken. chicken. Gallus gallus Gallus yotae; mitochondrial eukaryotes; Metazoa; Chordata; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NID KEYWORDS

RESULT 11
LOCUS
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GGU90541 Gallus ga U90541 g2213802

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VRT (GDNFRalpha)

25-JUN-1997 mRNA, complete

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                           CCCAGCTGCAGCTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGATTA
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                     CCAAGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCTATTA
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BASE COUNT 773
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                 CCTAAATGATACCTGCAAGAGGTTCAGATCTGCTTACATAACCCCCTGCACCAGCAGCAC 1281
                                                                                     --AGCCAGT--A-CT-AT--CAAAGGGGAACAACTGCTTGGATGCAGCAAAAGCTTGTAA
                                                                                                                                                    ACCAGTTAACAGCAGGCTATCAGACATATTCAGGCTAGCACCGATTGTATCAG-TGG---
                                                                                                                                                                                                                         GGCGACGGGCCTGGAGGCGAAGGATGAATGCAAAAGCGCCATGGAGGCTCTCAAGCAGAA 993
                                                                                                                                                                                                                                                                                                                                                                                                              CAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTCAGCCT
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CCTCGACGACATTTGCAAGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACCAGCGT
                                                                                                                                   ACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTCATATCAGATGTTTT
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Buj-Bello,A., Adu,J., Pinon,L.G., Horton,A., Thompson,J.,
Rosenthal,A., Chinchetru,M., Buchman,V.L. and Davies,A.M.
Neurturin responsiveness requires a GPI-linked receptor and the Ret
receptor tyrosine kinase
Nature 387 (6634), 721-724 (1997)
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Bute Medical Buildings, St. Andrews,
Location/Qualifiers
1, .3037
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Similarity 81.8%;
868; Conservative
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/db_xref-"FID: 92213803"

/db_xref-"PID: 92213803"

/translation-"MFLALLYLALPLADVLLSAEVSGLPGGDRLDCVKASDQCLKEQS

/translation-"MFLALLYLALPLADVLLSAEVSGLPGGDRLDCVKASDQCLKEQS

CSTKYRTLRQCVAGKESNFSRATGLEAKDECKSAMEALKQKSLYNCRCKRGMKKEKNC

LRIYWSMYQSLQGNDLLEDSPYEPVNSRLSDIFRLAPIVSVEPVLSKGNNCLDAAKAC

RLNDTCKRFRSAYITPCTSSTSNEICNKRKCHKALRLFFDKVPPKHSYGMLFCSCRDV

ACTERRQTIVPVGSYEEREKPNCLNLQDSCKKNYICRSRLADFTNCQDESRSVSSC

LKENYADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNGNDIDECRFLNFFQDN

TCLKNALQAFGNOTDVNVMQPILPVQTTTATTTASRLKNTGSETTNNELFTHNDSPA

CANLQACKKRKSNESVDTELCLNENAIGKDNTPGVSTSHISSENSFALPTSFYPSTPL
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/db_xref="taxon:9031"
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Pred. No. 0.00e+00;
0; Mismatches 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (complete cds. AF038420
                                                                                                Direct Submission
Direct Submission
Submitted (12-DEC-1997) Genetics, Case Western Reserve, Adelbert Road, Cleveland, OH 44106-4955, USA
Location/Qualifiers
                                                                                                                                                                                                                     Angrist, M., Jing, S., Bolk, S., Bentley, K., Nallasamy, S., Halushka, M., Fox, G.M. and Chakravarti, A.

Human GFRA1: Cloning, mapping, genomic structure, and evaluation a candidate gene for Hirschsprung disease susceptibility

Genomics 48, 354-362 (1998)
                                                                                                                                                                   2 (bases 1 to 832)
Angrist,M., Jing,S., Bolk,S., Bentley,K.,
Halushka,M., Fox,G.M. and Chakravarti,A.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
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1 (bases 1 to 832)
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                             /chromosome="10"
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join(AF038410:1. .314,AF038411:111. .396,AF038412:76.
AF038413:162. .245,AF038414:131. .145,AF038415:147. .
                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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GPI-linked
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(GFRA1) gene, exon
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Best Local Similarity 94.2%;
Matches 733; Conservative
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                                                        AGAAGGCTTTGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACTTGGGCTGTAAAGCA 498
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/gene="GFRA1"
/product="GFP - linked anchor protein"
/product="GFP - linked anchor protei
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/db_xref-"FIP: 92921545"
/db_xref-"FID: 92921545"
/translation-"MELATLYFALPILDILLSAEVSGGDRLDCVKASDOCLKEQSCST
/translation-"MELATLYFALPILDILLSAEVSGGDRLDCVKASDOCLKEQSCST
KYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCRCKRCMKKEKNCLRI
YWSMYQSLQGMDLLEDSFYEFVNSRLSDIFRVVFFISDVFQOVELIFRGNUKCLDAAKA
CNLDDICKKYRSAYITFCTTSVSNDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRD
IACTERRRQTIVFVCSYEEREKNCLNLQDSCKTNYICRSRLADFFTNCQFESRSVSS
CLKENTADCLLAYSGLIGTVMTPNYIDSSSLSVAFWCDCSNSGNDLEECLKFINFFKD
NTCLKNAIQAFKLKSNYSGLIGTVMTPNYIDSSSLSVAFWCDCSNSGNDLEECLKFINFFKD
NTCLKNAIQAFKLKSNYSGNTHLCISNGNYEKEGLGASSHITTKSMAAFPSCGLSFLLVL
PVTALSTILSITETS"
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Pred. No. 2.25e-297;
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  -GATTTTAACAGTTTTACTTCTGGCCTTTCCTAGCTA 579
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                                                                               CAAGAGTGGGCTTTGTGGAAACAGCTGGTACTGATGTTCACCTTTATATATGTACTAGCA
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                                        TTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGAGAACTACGCAG
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                                                                                                                          661;
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Submitted (08-JUL-1997) Laboratorio
Istituto Glannina Gaslini, Largo G.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
AF012811
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 777)
Puliti, A. and Seri, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                     Similarity
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                                                                                                                         19.3%;
llarity 84.9%;
Conservative
                                                                                                                                                                              ω
                                                                                                                                                                            from Soares mouse
Consortium"
                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
/clone-"402011"
/note-"EST deposited under GenBank Accession Number W76716
from Soares mouse embryo NbME13.5 14.5 cDNA library; IMAGE
                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
1. .430
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GDNF
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                                                                                                                         Score 488; DB 23;
Pred. No. 2.39e-295;
0; Mismatches 107;
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slini, 5, Genova 1614
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                                                                                                                                             Length 777;
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Angrist,M., Jing,S., Bolk,S., Bentley,K., Nallasamy,S.,
Halushka,M., Fox,G.M. and Chakravarti,A.
Human GFRA1: Cloning, mapping, genomic structure, and evaluation a candidate gene for Hirschsprung disease susceptibility Genomics 48, 354-362 (1998)
2 (bases 1 to 596)
Angrist,M., Jing,S., Bolk,S., Bentley,K., Nallasamy,S., Halushka,M., Fox,G.M. and Chakravarti,A.
                                                                                                    Direct Submission
Submitted (12-DEC-1997) Genetics,
Adelbert Road, Cleveland, OH 4410
Location/Qualifiers
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147. .483
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/gene-"GFRA1"
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44106-4955, USA
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2 (bases 1 to 385)

Angrist, M., Jing, S., Bolk, S., Bentley, K., Nallas Halushka, M., Fox, G.M. and Chakravarti, A.

Direct Submission

Submitted (12-DEC-1997) Genetics, Case Western Submitted (12-Decentics) Genetics, USA
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AF038410
g2921533
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1 (bases 1 to 385)

Angrist,M., Jing,S., Bolk,S., Bentley,K., Nallasamy,S.,
Halushka,M., Fox,G.M. and Chakravarti,A.

Human GFRAI: Cloning, mapping, genomic structure, and evaluation
a candidate gene for Hirschsprung disease susceptibility
Genomics 48, 354-362 (1998)
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Eukaryota; Metazoa; Chordata; Vertebrata;
Drimates; Catarrhini; Hominidae; Homo.
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156 c
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/db_xref="taxon:9606"
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GPI-linked
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Score 298; DB 22;
Pred. No. 7.33e-168;
0; Mismatches 0;
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Pred. No. 3.42e-195;
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AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTAA 77

rch completed: Wed Jun 24 19:01:51 1998 time : 5592 secs.

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MPgr Run on:

ular output not generated Wed Jun 24 20:29:12 1998; MasPar time 376.73 Seconds 868.165 Million cell updates/sec

>US-08-866-354-1 (1-2568) from US08866354.seq 2525

Description: Perfect Score: N.A. Sequence: Comp: 1 AATCTGGCCTCGGAACACGC......CACTCTTGTACAAAAGAAAA 2568 TTAGACCGGAGCCTTGTGCG......GTGAGAAACATGTTTTCTTTT

Scoring table: TABLE Gap 6 default

Nmatch STD Dbase 0; Query

Searched: 176886 seqs, 63680241 bases × N

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part22 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part55 36:part36 37:part37

tistics: Mean 9.999; Variance 6.681; scale 1.497

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11 13 14	10987654321	Result No.
39 39 38	1137 612 226 131 124 124 90 90	Score
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Oligonucleotide probe Base substituted E.co Generic DNA sequence Generic DNA sequence	Rat glial cell derive Mouse GDNFR alpha clo Mouse GDNFR alpha clo Human EST-derived seq Human EST-derived seq DNA probe 32 detects Human EST-derived seq Human EST-derived seq Base substituted E.co Oligonucleotide probe	Description
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T04613 T04613 T01567 T62359 N81538	T22691 Q62924 Q70473 T76233 T76270 Q59427	176363 176405 176452 176472 176405	Q70470 Q70471 Q70472 Q70473 Q70466 Q70466 Q70470	Q70468 Q70465 Q70466 Q70466 Q70467 Q70468 Q70468
Type A insertion gene 5' flanking region of Hamster cDNA probe sp Schizosaccharomyces p Sequence of a gene fr	n gene signa amoyl-phosph ric DNA seque n IL6 antise n MDNCF anti	Human interleukin 8 a Human endothelin-1 an Chymase antisense oli Generic DNA sequence Human endothelin-1 an	DNA sequen DNA sequen DNA sequen DNA sequen DNA sequen DNA sequen	Generic DNA sequence
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ALIGNMENTS

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isolated glial cell derived neurotrophic factor receptor alpha-
gray useful to develop products to diagnose and treat associated
disorders, particularly enteric nervous system or kidney disorders
disorders, particularly enteric nervous system or full-length rat glial cell derived neurotrophic
factor receptor alpha (GDNFR alpha) (see W27327), a novel
disorder for GDNF. It was isolated by expression cloning.
A cDNA library obtained from ventral midbrain tissue of E14 rat
cembryos was generated in a cytomegalovirus-based vector. cDNA
colones were transfected into COS 7 cells and expression of
putative GDNF receptors was detected by binding of iodinated GDNF.
A single positive pool was obtained, from which the cDNA clone was
closed to disorder the cDNA cone was detected by binding the cDNA can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T84975 standard; cDNA; 2378 BP.
T84975;
T84975;
27-APR-1998 (first entry)
Rat glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; rat; kidney disease; glomerulonephritis; therapy; ds.
                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
Klein RD, Moore MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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produce GDNFR alpha in transformed host cells. The invention relates to novel uses of GDNF and its receptor. In particular, it relates to native rat GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antibodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNFR alpha, systems for identifying GDNF-related conditions, methods for identifying molecules homologous to GDNFR alpha, and therappeutic techniques (claimed) for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system related disorders. Transgenic and knockout animals are also
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PN W09733912-A2.

PD 18-SEP-1997; U04363.

PF 13-MAR-1996; US-618236.

PR 14-MAR-1996; US-618902.

PR (GETH) GENERNTECH INC.

PR 14-MAR-1996; US-618902.

PR (GETH) GENERNTECH INC.

PI useful to develop products to diagnose and treat associated disorders particularly enteric nervous system or kidney disorders whi; PT useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders products to diagnose and treat associated for useful to develop products to diagnose and treat associated for memperature of the clone of kidney disorders products to network foll; 100pp; English.

CC This cDNA sequence comprises the 3' end of mouse full-length (CC gilla) coll derived neurotrophic factor receptor alpha (GDNFR alpha) (CC gene 25; the 5' end of the clone is given in CC grate GDNA (see T04975) as probe. The invention relates to native rat GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and CC antibodies which bind to the GDNFR alpha, including agonist and CC derivatives (extracellular domain), chimeric GDNFR alpha and soluble derivatives (extracellular domain), chimeric GDNFR alpha and cC therefore the conditions as well as various uses for these conditions, for detecting ligands cc GDNF diagnostic techniques for studying the physiological role of CC GDNF diagnostic techniques for studying the physiological role of CC GDNF diagnostic techniques for identifying GDNF-related conditions, and conditions, particularly kidney disease conditions, particularly kidney disease conditions and conditions, particularly kidney disease conditions and conditions are also cclaimed disease conditions.
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GDNF; mouse; kidney disease;
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nes 726; Conservative
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s; kidney disease; glomerulonephritis; therapy; ss.
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         CC This CDNA sequence comprises the 5' end of mouse full-length CC glial cell derived neurotrophic factor receptor alpha (GDNFR alpha) CC (see W27327) clone 26; the 3' end of the clone is given in CT 84977. Clone 26 was isolated from a mouse cDNA library using CC rat GDNFR alpha cDNA (see T84975) as probe. The invention relates CC to novel uses of GDNF and its receptor. In particular, it relates CC to native rat GDNFR alpha (see W27327), its variants and soluble CC derivatives (extracellular domain), chineric GDNFR alpha and CC neutralising antibodies, as well as various uses for these CC doubtes. It also relates to assay systems for detecting ligands CC molecules. It also relates to assay systems for detecting ligands CC GDNFR alpha, systems for identifying GDNF-related conditions, methods for identifying molecules for identifying GDNF-related conditions of CC GDNFR alpha, related conditions, particularly kidney disease CC associated with glomerulonephritis and enteric nervous system CC claimed. Als en. 70 %. 110 C. 150 C. 70 m.
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Mouse GDNFR alpha clone 26 5' end.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.
                                                                                                                                                                                                                                                                                                    Isolated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disord Example 1; Page 60; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
Klein RD, MOORE MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
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This DNA sequence comprises a human EST-derived sequence designated CY 170al0.rl. It can be used to identify gilal cell derived CY 170al0.rl. It can be used to identify gilal cell derived CY 170al0.rl. It can be used to identify gilal cell derived CY 170al0.rl. It can be used to identify gilal cell derived CY 170al0.rl. It seems to receptor (GDNFR) sequences, including human CY 170al0.rl. It seems to receptor GDNFR sequences are another CY 170al0.rl. It seems to result of these EST-derived sequences (see T84980-81) or CY 170al0.rl. It seems to relates to native rates to compress them. The invention relates to native rates CY 170al0.rl. It seems to relates to native rates CY 170al0.rl. It seems and soluble derivatives CY 170al0.rl. It seems to seem the derivatives CY 170al0.rl. It seems to see the semicons which CY 170al0.rl. It seems to see the compress to the CY 170al0.rl. It seems for the GDNFR alpha, including agonist and neutralising CY 170al0.rl. It seems for the sems for detecting ligands to GDNFR alpha, and set of GDNFR alpha, and set of GDNFR alpha, including seems for conditions, methods for the treatment of GDNF-related conditions, methods for the treatment of GDNF-related and GDNFR alpha-related CY 170al0.rl. It seems to conditions, particularly kidney disease associated with CY 170al0.rl. It seems to condition and knockout animals are also claimed.

Sequence 453 BP; 86 A; 152 C; 121 G; 91 T;
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W09733912-A2.

18-SEP-1997.

13-MAR-1996; US-618236.

14-MAR-1996; US-618236.
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Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy;
expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated glial cell derived neurotrophic factor receptor alpha - useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders Example 1; Page 61; 100pp; English.
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Klein RD, Moore MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
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DR WPI: 97-470819/43.

DR WPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha - elevelop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders PT disorders, particularly enteric nervous system or kidney disorders PT disorders, particularly enteric nervous system or kidney disorders PT Stample 1; Page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence designated CC ye83h05.rl. It can be used to identify glial cell derived human EST-derived sequences for CDNFR sequences are another CC variants. Also suitable as probes for CDNFR sequences are another CC compression of these EST-derived sequences (see T8490), and CC fragments of these EST-derived sequences (see T8490), and CC fragments of these EST-derived sequences (see T8490), and CC gone alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which CC bind to the GDNFR alpha, including agonist and neutralising captaints are obluble derivatives (systems for identifying GDNF-related conditions, methods for techniques for identifying GDNF-related conditions, methods for cethods for the treatment of GDNFR alpha, and claimed conditions, particularly kidney disease associated with CC conditions, particularly kidney disease associated disorders.

CC Transgenic and knockout animals are also claimed.

CC Transgenic and knockout animals are also claimed.
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14-MAR-1996; US-615902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCTCTTCTGCTCCTGCCGGGACATCGCCTGCACAGAGCGGAGGCGACAGACCATCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST-derived sequence ye83h05.rl.

cell derived neurotrophic factor receptor alpha; GDNFR alpha;
human; kidney disease; glomerulonephritis; therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.2%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A, Ryan AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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Pred. No. 3.49e-59;
0; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 453;
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Length 351;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                proliferation capacity - and its components and derived antibodies, useful in diagnosing malignant tumours.

Claim 1, Page 73; 106pp; German.

The DNA shown is found in human or animal cells that have an unlimited capacity for unlimited cell proliferation or tumour formation. They have no ability to promote immortalisation of the cells, and are usually found in a DNA-proteth complex in the cell cytoplasm. The DNA is useful for detection of these complexes, and diagnosis of malignant tumours. Differentiation between cells with unlimited and only transient proliferation is possible. (See also Q85493-54)

Sequence 385 BP; 121 A; 83 C; 90 G; 91 T;
          27-APR-1998 (first entry)
Human EST-derived sequence yI70a10.rl fragment.
Glial cell derived neurotrophic factor receptor alpha;
GDNF; human; kidney disease; glomerulonephritis; therap
                                                                                                                                                                   1369
                                                                                                                                                                                                                                      1309
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10-JAN-1996 (first entry)
DNA probe 32 detects DNA-protein complex in immortal cells.
DNA-protein complex; detection; proliferation; tumour forma
diagnose; malignancy; biopsy; probe; ss.
                                                                                                 T84981 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BOEF ) BOEHRINGER MANNHEIM GMBH.
Abken H, Albert W, Jungfer H,
WPI: 95-067344/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-1995.
13-JUL-1994; E02307.
15-JUL-1993; DE-323727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 6
Q85526 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-protein complex characteristic of cells with unlimited liferation capacity - and its components and derived antib
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                                                                                                                                                                                                                                      GATCTCGCCTTGCGGATTTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAGCT 1368
                                                                                                                                                                                                                                                    | gatctcgccttgcagatttttttaccaactgccagccagagtcaaggtctgtcagcaact 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAAGGGAACAACTGCCTGGATGCAGCGAAGGCCTGCAACCTCGACGACATTTGCAAGA 1044
                                                                                                                                                                   GTCTAAAGGAAAACTACGCTGACTGCCTCCTCGCCTACTCGGGGGCTTATTGG
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                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                 DNA;
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92.9%;
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                                                                                                                                                                                                                                                                                             e 96; DB 15; Lend
... No. 2.63e-38;
... No. 2.63e-38;
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                               GDNFR alpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                               18-SEP-1997;
13-MAR-1997;
14-MAR-1996;
14-MAR-1996;
                                                                                                                                                                                                                                                                                                       27-APR-1998 (first entry)
Human EST-derived sequence ye83h05.rl fragment.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
13-MAR-1997; U04363.
14-MAR-1996; US-618903.
14-MAR-1996; US-615902.
(GETH ) GENENTECH INC.
Klein RD, Moore MW, Rosenthal A, Ryan AM;
WPI; 97-470819/43.
ISOlated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disord
                                                                                                                                                                                                                                               expressed sequence Homo sapiens. W09733912-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      T84980;
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Klein RD, Moore MW, Rosenthal A, Ryan
WPI; 97-470819/43.
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14-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atgctcttctgctcctgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAACTGCCTGGATGCAGCGAAGGCCTGCAACCTCGACGACATTTGCAAGAAGTACAGG 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
152; Consei
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                                                                                                                                                                                                                                                                                               tag;
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Pred. No. 8.55e-35;
0; Mismatches 44
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Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutation of molecules and screening.

Disclosure: p; English.

CR Random point mutations were introduced into the alpha fragment of
CE E. coli beta-galactosidase. The wild type sequence was obtained as of
CS ingle stranded template and an oligonucleotide was hybridised to
CS ingle stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC transcriptase and the molecules are misincorporated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS Example 1; Page 61; 100pp; English.

CT This DNA sequence comprises a fragment of a human EST-derived so gequence designated ye83h05.rl (see T84978). It can be used as CC a probe to identify glial cell derived neurotrophic factor receptor CC (GDNFR) sequences, including human variants. The invention relates ct novel uses of GDNF and its receptor. In particular, it relates CC (extracellular domain), chimeric GDNFR alpha and antibodies which CC (extracellular domain), chimeric GDNFR alpha and antibodies which CC (extracellular domain), chimeric GDNFR alpha and antibodies which CC bind to the GDNFR alpha, including agonist and neutralising CC relates to assay systems for detecting ligands to GDNFR alpha, can consist of constitutions for identifying GDNF-related conditions, methods for techniques for identifying GDNF-related conditions, methods for CC dentifying molecules homologous to GDNFR alpha, and claimed CC methods for the treatment of GDNF-related and GDNFR alpha related CC dentifying molecules homologous to GDNFR alpha, and claimed CC methods for the treatment of GDNF-related and GDNFR alpha related CC dentifying molecules homologous to GDNFR alpha, and claimed CC methods for the treatment of GDNF-related and GDNFR alpha related CC dentifying molecules homologous to GDNFR alpha, and claimed CC methods for the treatment of GDNF-related and GDNFR alpha related CC dentifying molecules homologous to GDNFR alpha, and claimed CC methods for the treatment of GDNF-related and GDNFR alpha related CC dentifying molecules homologous to GDNFR alpha, and claimed CC dentifying GDNF-related and GDNFR alpha and Claimed CC dentifying GDNF-related with CC dentifying GDNF-related disorders.
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Matches 15
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N81164;
O8-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                 (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J,
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base substituted 
E.coli beta galac
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03-APR-1987; US-034819.
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l Similarity 76.48;
152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   galactosidase alpha-fragment;
coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 19..69
                                                                                                                                                                                                                                                                                                                                                                                                                                              /function=multiple cloning site 187..204 /*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-galactosidase alpha-fragment.
se alpha-fragment; base substitutions;
                                                                                                                                                                                                                                                                                                         Koivula A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1188
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Pred. No. 8.55e-35;
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051746;
051746;
31-MAY-1994
                                                                                                                                                                                                          LT 11
Q51746
                                                                                                                                                                                                                                                           1608
                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-55 and 051747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                             (BECT ) BECTON DICKIN Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                  01-DEC-1993.
24-MAY-1993; 108325
26-MAY-1992; US-889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BECT ) BECTON DICKINSON Shank DD, Spears PA; WPI; 93-378844/48
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24-MAY-1993; 108325.
26-MAY-1992; US-889651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1552 TTAAAANTGCAATTCAAGCCTTTGGCAATGGCTCC-GATGTGACCGTGTGGCAGCCAGCC 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                      New oligo:nucleotide probes specific for Mycobacteria - detection and amplification of Mycobacteria nucleic acid
                                                                                                                       Synthetic.
EP-571911-A.
                                                                                                                                                         Oligonucleotide probe mKl4-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                   Q51746;
31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligo:nucleotide probes detection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-571911-A.
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Oligonucleotide probe MK14-A
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                                                                                                                                                                                                                                                                               13 vhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctcaag
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                                                                                                                                                                                                                                                           GCCTTCCCAGTACAGACCACCACTGCCACTACCACCACTGCCCTCCGGGTTAAG
3; Page 14; 23pp; English
                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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11; Conser
                                                                       BECTON DICKINSON CO
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                                                                                     US-889651
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                                                                                                                                                                                                           CDNA;
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Pred. No.
45; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific for Mycobacteria of Mycobacteria nucleic a
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Pred. No. 1.07e-09;
57; Mismatches 31
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3.52e-09;
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Best Local
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Random point mutations were introduced into the alpha fragment E. coli beta-galactosidase. The wild type sequence was obtained single stranded template and an oligonucleotide was hybridised it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can amplified and them expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Base substituted E.coli beta-galactosidase E.coli beta galactosidase alpha-fragment; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                occurred singularly in any given mutant. See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford
WPI; 88-279927/40.
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N81164;
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 653
                              151
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                                                                                            91
                                                                                                                                                         31
                                                                                                                                                                                                     Local
                                                                                                                                         rccbgcaggycgacbcyrraggnyccccgggywccgagcycgaayycdchvgccgymrtt 90
:||: || || || :| :| || :| || :| || :| || ::||
                              cncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                             GGTCTCCTTGCCCGCCACGCACTGCCTTAGCGTGCGGTACTTGGTGCTGCAGCTCTGCTC
                                                                                          thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnn 150
                                                                                                                         GCCTCCATGGCGCTGCGGCACTCATCCTTGGCCTCCAGGCCGGATGC-CAGGCTGAAGTT 714
CTTCAGGCACTGATCACTGGCTTTCACGCAATCCA
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                                                                                                                                                                                                                                                     204 BP;
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/function=multiple cloning
187..204
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Pred. No. 3.7
45; Mismatcl
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Pred.
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3.72e-08;
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                                                                                                                                                                                      60; Indels
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                                                                                                                                                                                                                                                    11 T;
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RESULT ID Q

Q70469 standard;

DNA; 114

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RESULT
ID Q7
AC Q7
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DE G6
KW T5
KW eff
KW ed3
SS
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PI Fowlkes DM, Kay BK;

PI Fowlkes DM, Kay BK;

PI Fowlkes DM, Kay BK;

PI Identifying proteins or peptide(s) which bind a ligand - by

recomprising a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

CC comprising a binding domain and an effector domain

PS Disclosure; Page 35; 255pp; English.

CC 070469 is a generic DNA sequence used to generate random TSAR peptide

CC THis generic formula can be represented as follows: X(TGC)(NNB)10-

CC (TGC)(NNB)52(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction

CC sites (X is not the same as Y) that are not specified further. This

CC sequence generates peptides that are cloverleaf in structure. Other

CC concatenated by these generic sequences are shown in R65150-54. TSARs are

CC concatenated by these generic sequences are shown in R65150-54. TSARs are

CC concatenated by triber comprises a linker peptides, comprising at least

CC two functional regions - a binding domain with affinity for a ligand and

CC active. They may further comprise a linker peptide between the 2 domains.

CC The oligonucleotides are also designed so that the expressed peptide

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

CC contains 2 or 4 cysteine residues positioned in, or flanking, the

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CC contains 2 or 4 cysteine residues of the cystem of the ception of the comprising

CC attive. They may be a second of the cystem of
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Q70467;
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01-FEB-1994; U00977.

01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.
Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding effector domain; concateneated heterofunctional protein; linked direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR peptide libra TSAR; totally synthetic; binding effector domain; concateneated heterofunctional protein; lin direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formation or in vivo antibody production. The TSARs are easil characterised and have designed activity allowing direct and
                                                                                                     05-APR-1995
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.

CC 070467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: x(NNB)16(TGC)(NNB)1Z(NNB)16(TGC)(NNB)1X x CC and Y are flanking restriction sites (X is not the same as Y) that are contained the specific peptides generated by these generic sequences are shown in 070466-68.

CC Other specific peptides generated by these generic sequences are shown in comprising at least two functional regions - a binding domain with cc affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The CC deliver a chemically or biologically active moiety, eg. metal ion, cradioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. composed the conformation of macromolecules, eg. complex methods of hybridoma formation or in vivo antibody production. CC direct and rapid detection in a screening process.
                                                                                       Synthetic.

W09640162-Al.

19-DEC-1996.

06-JUN-1996; U09306.

07-JUN-1995; US-4744;
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01-FEB-1993; US-013416.

30-DEC-1993; US-175500.

31-JAN-1994; US-189331.

(UYNC-) UNIV NORTH CAROLINA.

FOWLKES DM. KAY BK;
                                                                                                                                                                                                                   Human interleukin 8 antisense oligonucleotide. Asthma: airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                T76363 standard; DNA; 172 BP. T76363; 15-SEP-1997 (first entry)
                            Metzger WJ, Nyce JW; WPI; 97-051871/05.
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(UYEC-) UNIV EAST CAROLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 5; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of airway diseases such as asthma - by topically applying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rapid detection in a screening process. 114 BP; 0 A; 2 C; 2 G; 2 T;
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larity 4.5%;
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34; Misma
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Matches 4
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human interleukin 8, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. sequence 172 BP; O A; 35 C; 42 G; 39 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subject
Claim 5;
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  701
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                                                                                                                                                    821 CTTCATACCCCGCTTGCAGCGGCAGTTGTAGAGCGACTTCTGCTTCAGGGCCTCCATGGC 762
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                                                                        GCTGCGGCACTCATCCTTGGCCTCCAGGCCGGATGCCAGGCTGAAGTTGGTCTCCTTGCC 702
CGCCACGCACTGC
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45; Conservative
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Algorithm algorithm Seconds 1 Seconds 256 ATGTTTTCTTTT Pred. No. Pred. No. Pred. No. Pred. No. Pred. No. Pred. No. 1.7:9b_est5 25:9b_gss 25:9b_gss 0.00e+00 nous 0.00e+00 nous 0.00e+00 nous 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00 nous 0.00e+00 nous 0.00e+00 nous 0.00e+00 p_Br 0.00e+00 nous 0.00e+00	9.6 515 7 AA512935 nh91b04.sl NCI_CGAP_Br (7.0 631 7 AA518362 vil0d02.rl Barstead mo (7.0 446 5 AA38798 vil0b07.rl Ko mouse em (7.0 446 5 21 W53498 vil0b07.rl Ko mouse em (7.0 446 5 21 W53498 vil0b07.rl Soares mous (7.0 476 7 AA51836 7 nl0lc09.sl NCI_CGAP_Br (7.0 476 7 AA471183 vil0b07.sl NCI_CGAP_Br (7.0 476 7 AA780215 vilob07.sl vilob07.sl vilob07.sl vilob07.sl vil	Mean 12.402; Variance 3.221; scale 3.850 o. is the number of results predicted by chance to have reater than or equal to the score of the result being predicted by analysis of the total score distribution. SUMMARIES Query A Query Ouery Oue	544	Scoring table: TABLE default Gap 6 Nmatch STD: Dbase 0; Query 0 Searched: 1759237 seqs, 667866413 bases x 2 Post-processing: Minimum Match 08 Listing first 45 summaries	Run on: Wed Jun 24 19:02:10 1998; MasPar time 2788.51 Seconds 1230:107 Million cell updates/ Bular output not generated. Title: Description: Perfect Score: N.A. Sequence: 1 AATCTGGCCTCGGAACACGCCACTCTTGTACAAAAGAAAA Comp: TTAGACCGGAGCCTTGTGCGGTGAGAACATGTTTTCTTTT	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd MPsrch_nn n.a. • n.a. database search, using Smith-Waterman algorith	
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.07e-	.07e-	.07e-	.00e-	.07e-	.07e-	.00e-	.00e-	.07e-	.00e	.07e	.07e-	.05e-	.09e	.09e-	.09e	.09e-	.09e-	.09e-	.09e-	.09e-	.85e-	.58e-	.53e-	.35e-	.39e-	.30e-	.90e-	.38e-	.19e-	2.24e-73	.12e-

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Insert Length: 1735 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 460. Location/Qualifiers 1515 /organism="Homo sapiens" /note="vector: pT7T3D-Pac (Pharmacia) with a modified	Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	Includ. (bases 1 to 515) 1 (bases 1 to 515) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NRALIONAL CANCER INSTITUTE, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact. Pobort Strangbard, Ph. D.	EST. EST. human. Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	AA512935 515 bp mRNA EST 05-AUG-1997 nh91b04.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:965839, mRNA sequence. AA512935

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Local Similarity 98.8%;
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                                                           Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                       vil0d02.rl Barstead mouse 903363 5', mRNA sequence. AA518362
    Marra
                                                                                                                                                                                                                                                         AA518362
                                           Murinae; Mus.
                                                                                                                          nouse mouse
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Ases 1 to 631)
,M., Hillier,L.,
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/clone_11b="NCI_CGAP_Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
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(db_xref="taxon:9606"
                     to 631)
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  Dietrich, N., Dubuque, T.,
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CGTGGTGCGATTGCAGCAGCAGTGGCAATGACCTGGAAGATTGCCTGAAGTTTCTGAATT
                                              GGCTTATTGGCACAGTCATGACCCCCAACTACATAGACTCCAGTAGCCTCAGTGTGGCCC
                                                                          GACTGATTGGCACAGTCATGACTCCTAACTACATAGACTCCAGCAGCCTCAGTGTGGCGC
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Fax: 314 286 1810
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The WashU-HHMI Mouse EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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h quality sequence stop: 259.
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Pred. No. 0.00e+00;
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Marra, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.; Dubu, Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washbr-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w53498 465 bp mRNA md45e01.rl Soares mouse embryo NbME13.5 clone 371352 5', mRNA sequence.
                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                               MGI:232784
                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                            Contact: Marra M/Mouse EST Project
Washbrigton University School of Medicinep
Wash Park Parkway, Box 8501, St. L
                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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Best Local Similarity 89.0%;
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                                               clone 402011
W76716
                                                   me81h06.r1 Soares mouse embryo NbME13.5 14.5 Mus clone 402011 5', mRNA sequence.
house mouse.
Mus musculus
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/dev_stage="13.5-14.5dpc
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/strain="C57BL/6J"
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Fax: 314 286 1810
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/sex="unknown"
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/clone="402011"
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Washbu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Ld
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubl
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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AA573164
g2347692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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1CI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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Primates; Catarrhini; Hominidae; Homo.
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h quality sequence stop: 319.
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                                                                                                                                         /clone="IMAGE:1071779"
/clone_11b="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                                                          /organism="Homo sapiens"
/note="Yector: pT773D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. This library is the normalized version of
NCI_CGAP_BT1.1 Library was constructed by Bento Soares
and M. Fatima Bonaldo."
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62 c
                             Score 303; DB 9;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 338.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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Eukaryotae;
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                                                                                               /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a Mot I
polylinker; last strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT773
vector. This library is the normalized version of
NCI_CGAP_Brl.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."
/db_xref="taxon:9666"
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/clone="IMAGE:966736"
/clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
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Oncology Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5
Tel: 416 3403834
Fax: 416 3403453
Email: r.hawley@utoronto.ca
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Claudio,J.O., Llew,C.C. and Hawley,R.G.
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                                                                                                                                           Seq primer: -28ml3 rev2 ET from High quality sequence stop: 470 Location/Qualifiers
                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free ti
IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
Washur-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA-GACAAAAGA---AAACCAAGTATTCTGTCCCCTGTCCTTGTATATCTGAAAATC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTCCACCCTATTATCTTTAACAGAAACATCATAGCTGCATTAAAAAAATACAATATGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGCTGCCCTGTTGTCTGTATCATTGGCAGAA-ACAT-CGT-AGCTGCATCCAGTATGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAATGGTAATTATGAAAAAGAAGGTCTCG---GTGCTTCCAGCCACATAACCACAAAA 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGATAATGATTACGGAAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                     CTGTAAAGC 2209
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCAMACTCAGAAGGCTTTGGGATATGCTGTATTTTAMAGGGACAGTTTGTAACTTGGG
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                                                                       Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheri Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST project
Unpublished (1997)
                                                                                                                                                                                                                                                                         AA780215 487 bp mRNA
af52f08.sl Soares total fetus Nb2HF8
1035303 3', mRNA sequence.
AA780215
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370; Conser
Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
                                            Contact: Wilson RK
                                                                                                                                                                                                                 Homo sapiens
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llarity 75.7%;
Conservative
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/clone_lib="Soares mo'
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>^</u>
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Pred. No. 1.21e-216;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 g
              School of Medicine way, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse NML"
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               Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 478;
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                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                           cDNA clone
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.3%;
Best Local Similarity 97.7%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 TTTACTTTTGTAAAAGAGTGCAGAACTGTTTACAGTACATAAACATCAGCGTGGAAAATG
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Peiligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGAATCTTCATTGTGGCAAAAAAGCTTGGCATCAATGTAGGCTGAAATT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGTACATATATAAAGGTGAACATCAGTACCAGCTGTTTCCACAAAAGCCCCACTACTTGG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGAATCTTCTTTGTGGCAAAAAAGCTTGGCATCAATGTAGGCTGAAATT 2399
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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EST182778
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Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 278)
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 bp mRNA EST Jurkat T-cells VI Homo sapiens cDNA
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Pred. No. 3.56e-187;
0; Mismatches 3;
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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Best Local S
Matches 11
           TITLE
JOURNAL
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MEDLINE
                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                  y170a10.r1
H12981
                                                     Eukaryotae: Metazoa: Eumetazoa: Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteicht Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theri Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 521) Hillier.L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                               Nature 37
96026280
          The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic;
9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser, C.M. and Venter, J.C.
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larity 99.2%;
Conservative
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/db_xref="taxon:9606",
/clone_1tb="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
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/note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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89 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 118; DB 4; L
Pred. No. 3.32e-126;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone 43207
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, Rockville,
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                                                                                          Marra, M.,
                                                                                                                                                                       Osteichthyes;
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RESULT 13
LOCUS
DEFINITION
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ORGANISM
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                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Local Similarity 74.9%;
hes 209; Conservative
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Contact: Wilson RK
WashU-Merck EST project
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                            vu9dd10.rl Stratagene mouse skin
1210003 5', mRNA sequence.
AA727460
                                                                                                                                                                            Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                  g2745167
EST.
                                                                                      Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. La
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                Rodentia; Metazoa; Chordata; Vertebrata; Mam
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 439)
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                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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/clone="43207"
154 c 144 g 119
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Pred. No. 1.04e-121;
0; Mismatches 65;
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REFERENCE
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INITION
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Best Local S
Matches 20
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Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mary Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. Wilson,R.
                                           Eucharyotae; Metazoa; Chordata; Ver
Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 229)
Hillier,L., Clark,N., Dubuque,T.,
                                                                                                 Homo sapiens
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                                                                                                           constructed by Bento Soares and M.Fatima Bonaldo.
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larity 73.6%;
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/clone_11b="Stratagene mouse
/sex="females"
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/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
79 c 117 g 138 t
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CDNA clone 124377
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                                                                                   Vertebrata;
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                                                Elliston, K., Hawkins, M.,
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                                                                         Gnathostomata; Homo.
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                                      Marra, M.,
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Best Local Similarity 74.0%;
Matches 168; Conservative
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mx03e07.rl
                                  Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                             Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
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WashU-Merck EST Project
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/clone="124377"
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Pred. No. 1.12e-90
0; Mismatches 5
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Best Local Similarity 73.1%;
Matches 125; Conservative
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/tissue_type="Liver"
/lab_host="DH10B"
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Onit.

MPsrch_pp protein protein database search, using Smith-Waterman algorithm

8:: ular output not generated Tue Jun 23 18:25:59 1998; MasPar time 15.62 Seconds 456.576 Million cell updates/sec

Title: >US-08-866-354-2 (1-465) from US08866354.pep 3369

Sequence: Description: Perfect Score: MFLATLYFALPLIDLILSAE......PLLVLVVTALSTLLSLTETS 465

Scoring table: PAM 150 Gap 11

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 34.730; Variance 143.021; scale 0.243

Statistics:

score greater and is derived ŏ. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

NO.	Score 3184 96 86 86 86 86 86 86	94.5 22.666.885	1	DB 27 27 27 27 27 27 27 27 27 27 27 27 27	W27327 P800885 P815252 W43305 P70272 P70272 P70272 P70272 P70272 P70272 P70272 P70272 P70272	cription glial c glial c bohydra en antigen sequenc V-IIIb p -1 MA de
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8	86		171	10	R55857	¥
9	86		267	N	P94509	uence
10	86		446	22	W19681	ATM mutant Cl339T
11	86		478	w	P60309	Sequence of gag
12	87		504	ω	P93707	uence of
13	86		506	σ	R29704	gag gene decoded
14	86		512	N	R10866	gag r
15	87		514	ω	R15237	Fusarium oxysporum
16	86	2.6	521	23	W13053	HIV-2 provirus-encode
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18	86	2.6	524	27	W43304	
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13-MAR-1997. U04363.
14-MAR-1996. US-618236.
14-MAR-1996. US-615902.
14-MAR-1996. H.C.
(GETH ) GENENTECH INC.
Klein RD, MOOTE MW, ROSENTHAL A, Ryan AM;
WPI; 97-470819/43.
N-PSDB; T84975.
Isolated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorder Claim 1; Page 78-79; 100pp; English.

This protein comprises full-length rat glial cell derived neurotrophic factor receptor alpha (GDNFR alpha), a novel gPI-linked protein that is a ligand-binding component of the receptor system for GDNF. Its amino acid sequence was deduced from an isolated cDNA clone (see T84975). The invention relates to novel uses of GDNF and its receptor. In particular, it relates to native rat GDNFR alpha (see W27327), its variants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W27327 standard; Protein; 468 AA.
W27327;
W27327;
27-APR-1998 (first entry)
Rat glial cell derived neurotrophic factor receptor alpha;
GINF; rat; kidney disease; glomerulonephritis; therapy.
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Matches 43
New variants of lymphadenopathy associated virus (LAV) - used for prodn. of DNA, antigens and antibodies used in diagnosis of AIDS and pre-AIDS Claim 8; Fig 8A-81; 72pp; English.

LAV EL I (N80436) and LAV MA L (N80437) were isolated from the peripheral blood lymphocytes of patients. Different AIDS virus isolates concerned are designated by 3 letters of the patients name. Stable probes including
                                                                                                                                                                                                                                     P80885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antibodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNF, diagnostic techniques for identifying GDNF related conditions, methods for identifying molecules homologous to GDNFR alpha, and therapeutic techniques (claimed) for the treatment of GDNF related and GDNFR alpha related conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system
                                                                                                                                                                         16-DEC-1990 (first entry)
Sequence encoded by LAV MA L GAG gene
HIV; HTLV III; AIDS; diagnosis; vaccine;
Lymphadenopathy associated virus MA L.
W08707906-A.
                                                                                                                (INSP) Inst Pasteur.
Alizon M, Sonigo P,
                                                                                                                                     30-DEC-1987.
22-JUN-1987; E00326.
23-JUN-1986; EP-401380.
                                                                                         N-PSDB; N80437
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                                                                                                                                                                                                                                                                                                                                                                                             YIDSSSLSVAPWCDCSNSGNDLEECLKFLNFFKDNTCLKNAIQAFGNGSDVTVWQPAFPV
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larity 92.9%;
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27; Mismatc
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R15252;
12-FEB-1992 (first entry,
12-FEB-1992 (first entry,
Carbohydrate binding domain #9.
Carbohydrate binding domain #9.
Carbohydrate binding domain #9.
                                            US5695930-A.
09-DEC-1997.
05-AUG-1996; 692445.
10-NOV-1994; US-337670.
(KILP/) KILPARRICK T J.
(WEIN/) WEINSTEIN D E.
KIlpatrick TJ, Weinstein
WPI; 98-041291/04.
                                                                                                                                                                                                                                                                                                                               W43305 standard;
W43305;
01-APR-1998 (fi
p17 antigen of )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fuel gas and feed protein, have specified carbohydrate binding domain Claim 20; Page 45; Tapp; English.

This CBD is homologous to a terminal A region of Trichoderma reesel cellulases and effects binding of a protein to an insoluble cellulosic or hemicellulosic substrate. It is one of ten specific CBD's (see R15244-R15253) which correspond to the generic CBD formulae in R15242 and R15243. The CBD is incorporated into a fusion protein comprising a catalytic domain from a cellulase, e.g. a Bacillus endoglucanase, and optionally comprising a linking B domain from e.g. a fungal endoglucanase.

Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09117244-A.
14-NOV-1991. DK0124.
08-MAY-1991. DK0124.
09-MAY-1990; DK-001158.
09-MAY-1990; DK-001158.
(NOVO ) NOVO NCROISK A/S.
W01dike HF, Hagen F, Hjort CM, Hastrup
WPI; 91-353766/48.
                                                                                                                                                                                                                                                     p17 antigen of human immunodeficiency virus type 1. Immunoassay; HIV-1; human immunodeficiency virus type 1; saliva; immobilised; p17 antigen; detection; nitrocellulose support; ant Human immunodeficiency virus type 1.
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Local Similarity 41.9%;
tes 18; Conservative
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larity 35.0%;
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7.18e+01;
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Best Local
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05-JAN-1987; 100064.
06-JAN-1986; US-816645.
(HOFF) HOSEMANN-LA ROCHE AV
Kramer R, Reddy P, Shaber M
WPI; 87-207550/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uery Match
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P70272 standard;
P70272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the p17 protein antigen of human immunodeficiency virus type 1 (HIV-1). The invention relates to a method for detecting antibodies to HIV-1, which comprises contacting saliva from a fasting human with immobilised HIV-1 p17 antigen, preferably on a nitrocellulose-containing solid support, and detecting any antigen-antibody complex, optionally with a labelled second antibody. The method can be used to detected exposure of a mammal, especially a human, to HIV-1. Detecting anti-HIV antibodies in saliva is safer as HIV is not transmitted via saliva, as opposed to blood. The assay is simple and cheap to perform without laboratory equipment or trained personnel and can be performed at home by the saliva donor.
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HIV virus;
HIV virus;
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Polypeptide obtd. from HTLV-III gag-gene - used for detecting Polypeptide obtd. from HTLV-III gag-gene - used for detecting AIDS virus and for prepn. of vaccines giving protective immun Claim 3; Page 13; 39pp; English.

The sequence encodes the HIV virus 14 KDA gag precursor gene. The HIV virus gag protein or proteolytically derived products may be used as a vaccine against HIV virus infection (AIDS). See also N70427, N70428, N70429, N70430 and N70432.

Sequence 120 AA;
                                                                                                                                                                                                                                 04-FEB-1993 (first entry)
HTLV-IIIb pl7 sequence.
human immunodeficiency virus; HIV-1; HIV-2; glycoprotein;
epitope mapping; monoclonal antibody; Glic1; Glih3; B4F8;
  peptide
                                                   peptide
                                                                                                    peptide
                                                                                                                                                       peptide
                                                                                                                                                                                                           Human
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04-FEB-1993
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The sequence encoding the HIV virus 14 KDa
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Local Similarity 37.2%;
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11..25
  /label= #2
21..35
/label= #3
31..46
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12; M
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Pred. No. 8.45e+01
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RESULTING ACTION OF THE PRINCIPLE PR
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CI The synthetic peptides #1-13 were used in epitope mapping studies commoclonal antibodies against pl7. ELIGA plates were coated with recombinant pl7 (rp17) and peptides #1-13 (representing the complete sequence of HTLV-IIIb pl7). Antibodies Gilql and Gilh3 (which react with live HIV infected cells and recognise a glycoprotein contg. a complete gag amino acid sequence and having mol. wt. 150,000 or 90,000, respectively), bound strongly to rp17 but did not bind to any of the peptides tested. The claimed monoclonal antibodies which competitively inhibit Gilgl or Gilh3 are further defined by the fact that they do cont substantially bind to the peptides 1-13. The MAbs can be used to determine the number of HIV-infected cells, to purify gag antigens or can be coupled to a toxin for therapeutic use.
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Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                              R55851 standa
R55851;
07-DEC-1994
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06-AUG-1992.
22-JAN-1992;
22-JAN-1991;
12-JAN-1993; U00267.
23-NOV-1992; US-979966.
(HARD ) HARVARD COLLEGE.
ESSEX ME, Lee TH, Yu X;
WPI; 94-200178/24.
Treating HIV infection with mutant HIV matrix polypeptide produced by transfection with viral vector, inhibiting replication, assembly or infectivity of virus particles Disclosure; Fig. 1A-1F; 61pp; English.
                                                                                                                                                                                                                                                                   HIV-1 MA delta-5-16 mutant.
HIV-1; matrix protein; MA; gene therapy; AIDS; deletion mutant.
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                     09-JUN-1994
                                                                                                                                                                                                                                                 W09412513-A.
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Abraham P, Honnen WJ, Revesz
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larity 37.2%;
Conservative
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93
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86..115
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105..115
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51..65
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41..55
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121..132
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78..92
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Revesz K, Shang F;
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Pred. No. 8.45e+01
12; Mismatches 10
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RESULT IN PAGE 11 PAGE 12 PAGE
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R5587;
R5587;
R5587;

DT 07-DEC-1994 (first entry)
DE HIV-1 MA delta-105-114 mutant.
KW HIV-1; matrix protein; MA; gene therapy; AIDS; deletion mutant.
OS Human immunodeficiency virus type 1.
PN W09412513-A.
PD 09-JUN-1994.
PF 12-JAN-1993; U00267.
PR 23-NOV-1992; US-979966.
PA (HARD ) HARVARD COLLEGE.
PS ESSEX ME, Lee TH, Yu X;
PR 15-58EX ME, Lee TH, Yu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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WHI; 94-200178/24.

Treating HIV infection with mutant HIV matrix polypeptide - pref. Produced by transfection with viral vector, inhibiting replication, assembly or infectivity of virus particles. Subsclosure; Fig. IA-IF; 6lpp; English.

CHIV infection is treated by administering to a patient a mutated CHIV matrix (MA) protein using a viral vector. Preferred mutants Care those given in R55851-60. The deletion/substitutions of the mutants either lower the incorporation of Env protein in the viral Courants either lower the incorporation of Env protein in the viral Courants either lower the incorporation of Env protein in the viral Courants either lower the incorporation of Env protein in the viral Courant entry into uninfected cells, disrupt virus assembly, or disrupt virus entry into uninfected cells. The DNA sequence encoding MA Cis given in 066839 and the as sequence in R55850.
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                                                                                                                                                                                                                                                                                                                                                                                       P94509 standard; protein;
P94509;
10-MAR-1993 (revised)
19-JUN-1989 (first entry
                                                                                 02-FEB-1989.
21-JUL-1987; 724016.
21-JUL-1987; DE-724016.
(WOLF) Wolf H.
                                                                                                                                                                                                                                                                                                                                      19-JUN-1989 (first entry)
Sequence encoded by plasmid pUC18Xmnstop
Human immunodeficiency virus; AIDS; bacto
                             Soutschek-Bauer E, Motz M, WPI; 89-039954/06.
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16; Conservative
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Location/Qualifiers
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12; Misma
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Pred. No. 8.45e+01;
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bacterial lysate; HI
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8.45e+01;
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Fig. 97-012070/01.

New 1: 97-012070/01.

Nr. N-SSDB; T68764.

PT New 1: 150lated ataxia-telangiectasia gene - used to develop prods. for the study, diagnosis and treatment of ataxia-telangiectasia.

PT the study, diagnosis, and treatment of ataxia-telangiectasia.

CL laim 5; Page -; 1:53pp; English.

CC wind 5; Page -; 1:53pp; English.

CC wind 5; Page -; 1:53pp; English.

CC wind 6; Avid type sequence). The ATM gene of the invention, is located control the human genome at chromosome segment 11:022-23. Ataxia-telangiectasia control the human genome at chromosome segment 11:022-23. Ataxia-telangiectasia control the human genome at chromosome segment 11:022-23. Ataxia-telangiectasia control the human genome at chromosome segment 11:022-23. Ataxia-telangiectasia control treatment for the human genome at chromosome segment 11:022-23. Ataxia-telangiectasia control treatment region of the ATM gene. A-T control treatment for the ATM gene. A-T control treatment for the ATM gene. A-T control treatment for the ataxia treatment for the atax
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16-MAY-1996; US-441822.
16-MAY-1995; US-441822.
08-APR-1996; US-629001.
(KOHN) KOHN K I.
(UYRA-) UNIV RAMOT APPLII
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This sequence is that of the human immunodeficiency virus-1 (HIV-1) pl7 antigen which is expressed as a fusion protein with a few extra AAs on both ends. The antigen (Ag) can be used in a western blot analysis to detect HIV antibodies in serum or other body fluids. The prepn is both cheap and safe and the Ag is used directly as a bacterial lysate. The directly as a more sensitive and accurate than conventional western blot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATM gene; ataxia-telangiectasia; progressive genetic disorder; antibody; central nervous system; immune system; chromosomal instability; therapy; cancer predisposition; radiation sensitivity; cell cycle abnormality; multi-system disease; autosomal recessive; cerebellar ataxia; cerebellum; general motor dysfunction; purkinje cell; oculocutaneous telangiectasia; blood vessel; bulbar conjunctiva; facial skin; A-T; mutein.
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Pr 03-JUN-1988; US-202271.

Rr 30-JUN-1989; MO-07256.

Rr 31-JUL-1989; WO-U02415.

Rr 11-JUL-1989; WO-U02415.

Rr 11-JUL-1989; WO-U02415.

Rr 11-JUL-1989; WO-U02415.

Rr 199-358956/49.

Rr N-PSDB; N92575.

Rr N-PSDB; N925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acquired immune deficiency syndrome polypeptide(s) - obtd. by molecular cloning etc. and used for diagnosis and in vaccines against virus disease Example; fig 2: 135pp; English.

A comparison of N60287 with the cDNA of the HTLV-III genome revealed one particular clone, designated ps. 21 which contained a DNA sequence encoding this peptide (P60308) sequence. This approx. 2.2 kilobase covers the precursor gag region and encodes, 5' to 3', p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base pairs 3' to the gag region (see N60288).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of gag and p24gag.
HIV: LAV; AIDS; dlagnosis; vaccine.
HTLV-IIIB/H9 cells (ATCC CRL 8543).
Kev Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 12
P93707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1992 (first entry)
Sequence of the gag protein precursor.
Vaccine; diagnosis; AIDS; LAV; HTLV-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1985; 309454.
24-DEC-1984; US-685272.
04-DEC-1985; US-805069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P93707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; N60288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH II
Capon DJ, Lasky LA;
WPI; 86-177602/28.
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                               2.6%;
Local Similarity 37.2%;
nes 16; Conservation
  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
kyk-lkhivwasrelerfavnpglletsegcreilgql-qpsl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%;
Similarity 37.2%;
16; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label-
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133..478
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Pred.
12; M
                                        Score
Pred.
12; M
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                                            Mismatches
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                                                                87;
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8.45e+01
                                                                DB 3; I
7.18e+01;
                                          10;
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                                                                                  Length 504;
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                                            Indels
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Best Local S
Matches 1
                                                                                                                                                                                                  03-JUN-1988; US-202271.
11-JUL-1989; WO-U02415.
(SMIK ) SMITHKLINE BECKMAN C
Gheysen D, Jacobs E;
WPI; 91-051332/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R29704 stand:
R29704;
26-APR-1993
                                                                                                                                                                                                                                             11-JUL-1989;
03-JUN-1988;
11-JUL-1989;
Disclosure; Page 7; 40pp; English.

The protein is encoded by an exemplary coding region for the HIV gag precursor which lacks 3' and 5' flanking sequences. For expression in eucaryotic cells, the sequence is operatively linked to a regulatory element which functions in the selected host cells. Immunogenic particles comprising full-length gag precursor protein are immunologically similar to authentic gag particles. The protein is recognised by anti-p16, anti-p24 and anti-p17 antibodies and lacks functions required for viral maturation and replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct including replication system recognised by unicellular microorganism - used to form recombinant proteins for diagnosing AIDS and lymphadenopathy syndrome Example 5; Fig 2; 32pp; English.

This sequence was decoded from the gag gene from proviral hTLR DNA. Proteins associated with lymphadenopathy syndrome and/or AIDS may be used in serological immuno-assays to detect antibodies to hTLR. The polypeptides can be used alone or in fusion constructs to produce antisera or monoclonal antibodies which may be used for therapy or diagnosis.
                                                                                                                                      N. escoding HIV gag precursor - devo
DNA encoding HIV gag precursor - devo
regions and with regulatory, regions
cells, used for vaccine prepn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barr PJ, Dina D, George-Nascimento C, Hallewell
Luciw PA, Parkes D, Pescador RS, Steimer K, Truc
WPI; 92-417329/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gag gene decoded from viral DNA from hTLR express proteins; lymphadenopathy syndrome
                                                                                                                                                                                                                                                                                              24-JAN-1991.
                                                                                                                                                                                                                                                                                                                            human immunc
WO9100904-A.
                                                                                                                                                                                                                                                                                                                                                      HIV gag precursor
                                                                                                                                                                                                                                                                                                                                                                                       R10866
                                                                                                                                                                                                                                                                                                                                                                                                     R10866 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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06-SEP-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human T cell lymphotropic retrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serological immunoassays;
                                                                                                                                                                                                                                                                                                           J03049686-A (non-conventional equivalent).
                                                                                                                                                                                                                                                                                                                                                                      17-APR-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 KYRTLRQCV-AGKETN-FSLASGL-EAKDECRSAMEALKQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYRTLRQCV-AGKETN-FSLASGL-EAKDECRSAMEALKQKSL
                                                                                                                                                                                                                                                                                                                                        immunodeficiency virus; HIV; gag protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 AA;
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US-696534.
US-773447.
                                                                                                                                                                                                                                                                               U02415
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Pred.
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                                                                                                                                                        devoid of natural flanking ions for expression in eukaryotic
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No. 8.45e+01
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Truett
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                                                                                                                                                                                                                                                                                                                                           AIDS
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Rest Local S
atches
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14-NOV-1991; DK0124.

08-MAY-1991; DK-001158.

09-MAY-1990; DK-001158.

(NOVO ) NOVO NORDISK A/S.

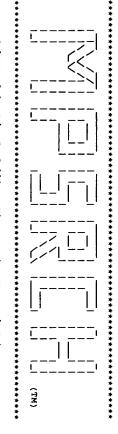
WOldike HF, Hagen F, Hjort CM, Hastrup S;

WPI; 91-353766/48.

N-PSDB; Q14838.

N-PSDB; Q14838.
                                                                                                                                                               binding domain
Claim 1; Fig 11; 73pp; English.
Claim 1; Fig 11; 73pp; English.
The full-length C-family cellobiohydrolase coding sequence was
The full-length C-family cellobiohydrolase coding sequence was
isolated from a F. oxysporum cDNA library by hybridisation to PCR
generated genomic oligonucleotide probes (see esp. Q15502). The
enzyme encoded by the sequence has a CBD which is homologous to a
terminal A region of T. reesei cellulase and is able to bind to
insoluble (hemi)cellulosic substrates. See also Q14839-Q14842.
Sequence 514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R15237 standard; Protein; 514 AA... R15237;
R15237;
11-FEB-1992 (first entry)
Fusarium oxysporum C-family cellobiohydrolase.
cellulose; carbohydrate binding domain; CBD; fungi; cellulase.
Fusarium oxysporum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It can
                                                                                                                                                                                                                                                                                                                                     New fungal (hemi) cellulose degrading enzymes - for prodn. of liq. fuel gas and feed protein, have specified carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                             496 tckspftck-kindfysqcq 514
:||::||::||::||
249 SCKTNYICRSRLADFFTNCQ 268
                                                                                                               2.6%;
Local Similarity 35.0%;
nes 7; Conservative
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Local Similarity 37.2%;
hes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used as a diagnostic agent for detection of exposure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
483..514
/label- CBD
/note- "homologous to a terminal A region of T.reesei cellulase"
                                                                                                                             Score 87; DB 3; 1
Pred. No. 7.18e+01
8; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 2; Length 512; Pred. No. 8.45e+01; 12; Mismatches 10; Indels
                                                                                                                                                          Length 514;
                                                                                                                               4; Indels
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                                                                                                                             Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Tue Jun 23 18:23:39 1998; MasPar time 23.53 Seconds 721.817 Million cell updates/seconds

Title: >US-08-866-354-2
Description: (1-465) from US08866354.pep
Perfect Score: 3369
Sequence: 1 MFLATLYFALPLLDLLLSAE......PLLVLVVTALSTLLSLTETS 465

Scoring table: PAM 150 Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 46.109; Variance 80.746; scale 0.571

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	BB	Ħ	Description	Pred. No.
Р	171	5.1	24	2	569080	glycosyl-phosphatidyl	3.50e-13
N	102		249	N	89860S	Ç.	1.21e-01
w	101	3.0	. 352	ν	S60024	_	1.68e-01
4	98		346	N	A70144	hypothetical protein	4.43e-01
u	93		169	N	I64089	protein-export protei	
σ	95		336	N	D70030	alkanal monooxygenase	1.15e+00
7	94		411	N	н69158	LPS biosynthesis RfbU	1.56e+00
æ	93		600	N	S07638	spore coat protein SP	2.13e+00
9	95		706	N	S62933	hypothetical protein	1.15e+00
10	96		826	N	A60385	-	8.37e-01
11	95		857	N	S33821	median body protein -	1.15e+00
12	94		1075	N	S54067	probable membrane pro	1.56e+00
13	91		475	N	S49886	membrane	3.92e+00
14	92		493	N	JC5621	l growth f	2.89e+00
15	92		563	_	VCMVM7	env polyprotein - bab	2.89e+00
16	92		889	ب	Clhus	complement subcompone	2.89e+00
17	92		695	N	805008	serine proteinase, ca	2.89e+00
18	86		120	თ	1TAM	hiv-1 matrix protein	1.71e+01
19	98		167	N	C64361	hypothetical protein	1.71e+01
20	86		316	N	S58719	~	1.71e+01
21	89		327	N	A55356	urokinase-type plasmi	7.12e+00
22	87		342	N	S42885	beta-1,3-glucanase (E	1.28e+01
23	86	2.6	387	2	B49175	Motch A protein - mou	1.71e+01

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34 4	ω ω	32	31	30	29	28	27	26	25	24
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2531	2471	1407	1403	1403	1182	1146	1033	769	646	642	522	521	521	521	512	506	502	500	494	491	478
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S18188	A49128	A41089	JQ1397	S24548	A35962	B35962	S54506	JC1121	S36586	G69371	FOLJGG	S12152	S53091	FOLJST	FOVWH3	A38068	FOVWA2	FOVMLV	G64382	S49779	FOVWVL
notch protein homolog	e determini	neuronal precursor pr	-	homeotic protein pros	protein-tyrosine kina	protein-tyrosine kina	probable membrane pro	leukocyte adhesion pr	tein	4		-		polyprotein -	polyprotein -			gag polyprotein - hum	acetolactate synthase	2	gag polyprotein - hum
1.28e+01	1.28e+01	9.56e+00	9.56e+00	٠	٠	1.28e+01	7.12e+00	1.71e+01	1.71e+01	1.28e+01	9.56e+00	1.28e+01	9.56e+00	9.56e+00	1.71e+01	9.56e+00	1.71e+0	1.71e+0	9.56e+00	7.12e+0	1.71e+0

ALIGNMENTS

#journal #title	ACCESSIONS REFERENCE #authors	ORGANISM #note DATE	RESULT 2 ENTRY TITLE	Db 1 MFLATL Qy 1 MFLATL	Query Match Best Local Sim Matches 23;	#accession ##status ##molecule_ ##residues SUMMARY	#journal #title	ACCESSIONS · REFERENCE #authors	ORGANISM DATE	RESULT 1 ENTRY TITLE
1, T.; Hutchison III, C.A.; AA.; Preddle, E.; Satchwell, ton, K.M.; Barrell, B.G Immunol. (1990) 154:125-16 ein-coding content of the se	, אל 	#formal name human cytomegalovirus, human herpesvirus 5 host Homo sapiens (man) 07-Sep-1990 #text_change	S09868 #type complete hypothetical protein UL103 - human cytomegalovirus (strain AD169)	MFLATLYFALPLLDLLMSAEVSGG 24		S69080 Preliminary type mRNA 1-24 ##label TRE 1-24 #molecular-weight 2573 #checksum	Beck, C.I Hefti, F uj-Bello, Vandlen, 2:80-83 of a muli	13 MAI 1990 869080 869080 Treanor, J.J.S.; Goodman, L.; de Sauvage, F.; Stone, D.M.;	rat #formal_name Rattus norvegicus #common_name Norway rat 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change	S69080 #type complete glycosyl-phosphatidylinositol-linked protein GDNFR-alpha -

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ACCESSIONS
REFERENCE
#authors
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ENTRY
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Best Local Similarity 26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
    #journal
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##residues 1-320 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 CTTSVSNDVCN-RRKCHKALRQFFDKVPAKHSYG-MLFCSCRDIACT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 CTVISCVENCNLTRKCLHDLLQYLDAVNVRESFGRLLHHSARRLICS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##cross-references EMBL:U20507; NID:g1041820; PID:g1041821
NDS G protein-coupled receptor; transmembrane protein
% #length 352 #molecular-weight 39503 #checksum 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AILFFNCHILA-SLRRRGERVPSRCG-GPRDSKSTALIL-TLVASFLVCWAPYHFFAFLE
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##note this sequence was submitted to the EMBL Data Library,
December 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 CLWQVHAIGGCFWEEFTDLGLQLSNFSAFVNSCLNPVIYV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GMLFCSCRDIACTERRRQTIVPV-CSYEERE-KPNCLNLQDSCKTNYICRSRLADF-FTN 266
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Local Similarity 36.2%;
nes 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQPESRSVSSCLKENYAD-CL-LA-YSGLIGTVMTPN-YI 302
Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dodsherty, B.; Tomb, J.F.; Freischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artlach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Nature (1997) 390:580-586
                                                                                                                                                                                                                                                                          spirochete
13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change
13-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MacNeil, T.; Bierilo, K.K.; Menke, J.G.; Hess, J.F. Biochim. Biophys. Acta (1995) 1264:223-228 Cloning and pharmacological characterization of a rabbit bradykinin B(1) receptor.
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hypothetical protein BB0354 - Lyme disease spirochete
#formal_name Borrelia burgdorferi #common_name Lyme d
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#formal_name Oryctolagus cuniculus #common_name domestic
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Pred. No. 1.68e-01
32; Mismatches 3:
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Pred. No. 1.21e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
ecosesics references MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                            #description
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##residues 1-169 ##label TIGR
##cross-references GB.U32758; GB:L
    305 SSLS
                                           135 LNLS 138
                                                                                      246 LQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYS-GLIGTVMTPNYIDS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
##residues 1-3
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Y #length 346 #molecular-weight 41137
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                                                                                                                               75 LEDSGDVAFICEVKQAGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLVNRGTFPA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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Similarity 31.98;
15; Conservation
                                                                                                                                                                          h 2.8%;
Similarity 25.0%;
16; Conservative
    308
                                                                                                                                                                                                                                                                                                   one of the proteins required for the normal export of envelope proteins out of the cell cytoplasm; may be involved in the initiation of the exporting process #superfamily protein-export protein secB
                                                                                                                                                                                                                                                               protein export
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164089
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Pred. No. 4.43e-01
11; Mismatches 1
                                                                                                                                                                          Score 93; DB 2; Le
Pred. No. 2.13e+00;
17; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:L42023; NID:g1573747; PID:g1573750;
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1-336 ##label KUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 NSGEDFPEQLEELRNYFKPSGNVRNQVRAIPGEGIDVPIW 171
                                                                                                                                                                                                                                                                                                                                                                                                     317 NSGNDLEECLKFL-NFFKDNTCLKNAIQAF-GNGSDVTVW 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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Similarity 42.5%;
17; Conservative
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Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Chol, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, F.T., Grandi, G.
                                                                                                      H69138 #type complete
LPS blosynthesis RfbU related protein - Methanobacterium
thermoautotrophicum (strain Delta H)
#formal_name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily ynbW protein
#length 336 #molecular-weight 37101 #checksum
                                                                           05-Dec-1997
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Pred. No. 1.15e+00;
11; Mismatches 10: Tndola
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                                              ##molecule_type mRNA
##residues 1-155,'T',157-414,'C',416-600 ##label TA2
                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-600 ##label FOS
##cross-references EMBL:X16491; NID:g7373; PID:g295736
                                                                                                                                                        ##residues
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##cross-references GB:AE000666
                                                                                                          ##status
                                                                                                                                                        ##residues 1-155,'T',157-414,'C',416-600 ##label TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 IESLKDLELDDVKCIILGAPVDEEYLRTLRGLAESMDSDVEFFGPVPYTEVPTWMNAADV 311
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Local Similarity 24.38;
es 18; Conservation
                                                                                                                                                                                                Cell Differ. Dev. (1990) 31:1-9
Isolation and characterization of spore coat protein (sp96)
gene of Dictyostelium discoideum.
A60942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fosnaugh, K.L.; Loomis, W.F.
Nucleic Acids Res. (1989) 17:9489
Sequence of the Dictyostellum discoldeum spore coat gene SP96.
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                                                                                                                                   B60942
22/1
duplication;
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#formal_name Dictyostelium discoideum
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
09-Sep-1997
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glycoprotein
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Pred. No. 1.56e+00;
26; Mismatches 25; Indels
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#title
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##molecule_type DNA
##residues 1-706 ##label AND
##tesidues 1-706 ##label AND
##cross-references EMBL:Z71297; NID:g1301850; PID:e239664;
##cross-references EMBL:Z71297
##cross-references EMBL:Z71297; NID:g1301850; PID:e239664;
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##molecule_type mRNA
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Local Similarity 26.6%;
nes 21; Conservative
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Similarity 40.4%;
19; Conservative
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S62920
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#formal_name Saccharomyces cerevisiae
27-Apr-1996 #sequence_revision 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the Protein Sequence Database, $62933
                                                                                                                                                                                   A60385 #type complete
monocyte surface antigen MS2 precursor - mouse
#formal_name Mus musculus #common_name house mouse
03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change
                 lineage.
A60385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers,
                                                                Molecular cloning
                                                                                  Int. Immunol. (1990) 2:585-591
                                                                                                                    Yoshida,
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#product spore coat protein SP96 #status predicted
#label MAT\
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#region 9 residue repeats\
#region 32 residue repeats\
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                   Setoguchi, M.; Higuchi,
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Pred. No. 1.15e+00;
23; Mismatches 31;
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Pred. No. 2.13e+00;
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                                              of cDNA encoding MS2 antigen, strongly expressed in murine m
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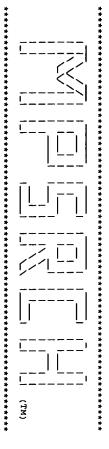
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Best Local Similarity 33.3%;
Matches 15; Conservative
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Best Local Similarity 33.3%;
Matches 17; Conservative
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659-683
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                                                                                       ##cross-references EMBL:249219; NID:g805025; ##experimental_source strain AB972 NCE S61058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 EHIPKGNNCLDAAKACNLDDICKKYRSAYITP-CTTSVSND-VCN-RRKCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:x13335
(FICATION #superfamily disintegrin homology
glycoprotein; surface antigen; transmembrane protein
##molecule_type DNA
#residues 465-1075 ##label BAW
##cross-references EMBL:268111; MIPS:YPR042c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 KENSYNFDQLLEQKQQMRSDLNALREKAADYE-RVDRELRLKDKE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-857 ##label MAR
##cross-references EMBL:X64517; NID:g312670; PID:g312671
## #length 857 #molecular-weight 100583 #check
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S33821
                                                                   Badcock, K.; submitted to
                                                                                                                                                                                                                                                                                                                                                 hypothetical protein YP3085.06c; hypothetical protein
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J. Mol. Biol. (1993) 231:521-530
Sequence and structure of a new of microtubule bundle in Giardia.
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median body protein - Giardia lamblia
#formal_name Giardia lamblia
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                                                                                                                                            S54067; S61063
                                                                                                                                                                                                                                                                                               #formal_name Saccharomyces cerevisiae 08-Jul-1995 #sequence_revision 26-Jul
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                                                                                                                                                                                                                           Badcock, K.;
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probable membrane protein YPR042c -
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#domain transmembrane #status predicted #label TMM\
#active_site Glu #status predicted
#active_site Glu #status predicted
jth 826 #molecular-weight 89896 #checksum 2686
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                                                                 Churcher, C.M.
the EMBL Data Library,
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Pred. No. 1.15e+00;
16; Mismatches 11
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Pred. No. 8.37e-01;
10; Mismatches 18
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Best Local Similarity 31.7%;
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Best Local Similarity 30.2%;
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                                                                                                                                                                                                                                                                                                                                                                294 CKNGYLYRSNTDADYLCEWGVEAAYVVSKLSKGVAICRTDYPG-TENMVIPTYVEGGSSL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 TLLITWLLDTCTLPNKNLILCDKLVN 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                679 SFIFESVLSHFWTIVQNRYGSRAVRACLEADSIITQCQLLTITSLI-IVLSPYLATDTNG 737
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A.; Sakiyama, S.; Nasamura, Y.; Ichimiya, S.; Na. Biochem. Biophys. Res. Commun. (1997) 237:245-250 Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5). JC5621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Y18277.06
#formal_name Saccharomyces cerevisiae
13-Jan-1995 #sequence_revision 20-Feb-1995
                                                                                                                                   JC5621 #type complete
epidermal growth factor-like protein, T16 - rat
#formal_name Rattus norvegicus #common_name Norway rat
09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
12-Dec-1997
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th 475 #molecular-weight 48070 #checksum 418
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Pred. No. 3.92e+00;
14; Mismatches 26; Indels.
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Best Local Similarity 25.6%;
Matches 10; Conservative
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282,292,306,312,
321,339,469
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437-449
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200-237,238-277,
278-318,319-359
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This protein plays a role in the regulation of cell growth by
interacting with DAN protein through DA41 protein.
    105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
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##residues 1-493 ##label OZA
                                       161 PIHVS-DGGGPLDTTRIKSVQRKLEEIHKAL-Y-PELQYHPLA-IPKVRDNL 208
                                                                                                                    103 YTSYQQCRSGNKTYYT-ATLLKTQTGGTSDVQVLGSTNKLIQSPCN-GIKGQSICWSTTA 160
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    SMYQSLQGNDLLEDSPYEPVNSRLSDIFRVVPFISDV-FQQVEHIPKGNNCL
                                                                              YRTLRQCVAGKETNESLASGLEAKDECRSAMEAL-KQKSLYNCRCKRGMKKEKNCLRIYW
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Similarity 21.4%;
24; Conservati
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env polyprotein - baboon endogenous virus (
coat polyprotein coat protein p20E
coat protein 9p70; coat protein p20E
#formal_name baboon endogenous virus
host Paplo sp. (baboon)
30-Jun-1992 #sequence_revision 30-Jun-1992
                                                                                                                                                                                                                                      #binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 563 #molecular-weight 61879 #checksum 3481
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The entire nucleotide sequence of baboon endogenous virus DNA: a chimeric genome structure of murine type C and
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#binding_site carbohydrate
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#product coat protein p20E *status predicted *label CPP\
#region immunosuppressive peptide *status predicted\
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13; Misma
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- baboon endogenous virus
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Pred. No. 2.89e+00;
32; Mismatches 48
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Search completed: Tue Jun 23 18:25:42 1998 Job time : 123 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Tue Jun 23 18:19:39 1998; MasPar time 15.99 Seconds 729.505 Million cell updates/sec

oular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-866-354-2 (1-465) from US08866354.pep 3369 1 MFLATLYFALPLLDLLLSAE.....

MFLATLYFALPLIDLLISAE......PLLVLVVTALSTLLSLTETS 465

Scoring table: PAM 150 Gap 11

Searched:

69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 47.888; Variance 65.919; scale 0.726

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2222111111008765432 3220987654321113210087654321	NO.
3335 31183 12593 12593 14522 1480 931 931 931 931 931 931 931 931 931 931	Score
66674444 000000000000000000000000000000000	Query Match
464 468 468 463 463 463 463 463 463 463 463 463 463	Length
	80
GDNR_HUMAN GDNR_MOUSE GDNR_CHICK NRTR_HUMAN NRTR_HUMAN NRTR_CHICK ULA3_HRABIT SECB_HAEIN SPA6_DICHO YNC1_YEAST YNC1_YEAST GAG_HV1NA GAG_	ID
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0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 0.00e+00 3.32e-03 3.39e-03 2.92e-01 1.38e-01 1.38e-01 4.23e-01 4.23e-01 4.23e-01 3.62e+00 3.00e+00	Pred. No.

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1 MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60

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ALIGNMENTS

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Matches 463	10021	Query Match	SEQUENCE	CARBOHYD	CARBOHYD	CARBOHYD	DOMAIN		PROPEP	CHAIN	SIGNAL	RECEPTOR;	MIM; 601496;	OTMIT ADTIV	-:- SUBCELLULAR	•	WITH T	-!- SUBUNIT: 2	SIMILARITY).		-!- FUNCTI	CELL 85:1113-1124(1996)		ANTONIO L.		MEDLINE; 9		UENCE		EUTHERIA;	EUKARYOTA; METAZOA;	HOMO SAPIENS	GONERA OR TRURI	NEUROTROPHIC FACTOR	01-NOV-1997	01-NOV-1997	01-NOV-199	P56159;	LT 1 GDNR_HUMAN	
463; Conservative			Ã,	405 4		59				25	щ	GLYCOPROTEIN;		DITTY: BELONCE		•	THE DISULFIDE-LINKED GDNF	T: 2 MOLEC	RITY).	AUTOPHOSPHORYLATION AND ACTIVATION OF	FUNCTION: RECEPTOR	13-1124(19		L., HU Z., CUPPLES R.,	WEN D., YU Y.,			FROM N.A.			TAZOA;	NS (HUMAN)				(REL.	(REL.		STANDARD	
•	٠	99.0%; s	51291 MW;	405	346	59	368		464	-ي	24	GPI-	č	NCC TO THE	LOCATION: ATT		IDE-LINKED	MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO		TION AND A	OR FOR GDNF.	96).		UPPLES R.	Y., HOLST		NIGRA;				CHORDATA; VERTEBRATA;			RECEPTOR 1)	LAST	LAST	CREATED)		OARD;	
0; M1:		Score 3	2C8C3574	POTENTIAL.	POTENTIAL.	POTENTIAL.	POLY-THR.	(POTENTIAL).	HYDROPHOBIC,	GDNF R	POTENTIAL.	ANCHOR;		d dance	ATTACHED		GDNF	DNFR-A		CTIVAT	ÑF. ME				P.L.,						VERTE		,	(GDNE	NOTATIO	SEQUENCE	ت		PRT;	
Mismatches	_	3335; [IAL.	IAL.	IAL.	HR.	FIAL).	HOBIC,	ECEPTOR	IAL.	MEMBRANE;		D FAMILY	THE		DIMER AND	LPHA AF			MEDIATES			LOUIS JC.,	LUO Y.,						BRATA;			K-ALPHA	ANNOTATION UPDATE	UPDATE)			464 2	
) S 1;		DB 1; I	CRC32;						REMOVED	GDNF RECEPTOR ALPHA.			•	₹	MEMBRANE		ND 2 MC	E THOU			THE GD!			SOH	FANG						TETRAPO			(TGF-BETA		S			AA.	
Indels	•	Length 4							DURING			SIGNAL.			2		2 MOLECULES	HT TO F		RECEPTOR	GDNF - INDUCED			r	M., TAMIR						TETRAPODA; MAMMALIA;									
1;		464;							MATURATION						GFT ANCHOR	27	OF RET	S R M		OR (BY	B				IR R.,						MALIA;			KELATED						
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 Query Match
Best Local S
Matches 43
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MEDLINE; 96270513.
JING S., WEN D., YU
ANTONIO L., HU Z., (
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
010NF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA I NEUROTROPHIC FACTOR RECEPTOR 1).
GDNFRA OR TRNR1.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M.
                                                                                                                                                                                            RECEPTOR;
SIGNAL
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YEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTT
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Similarity
430; Conse
                                                                                                                                                                                                         GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE;
94.5%;
llarity 92.9%;
Conservative
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59
347
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51649
                                                                                               369
59
347
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Score 3184; DB 1;
Pred. No. 0.00e+00;
27; Mismatches 5
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POLY-THR.
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6A7A2B2A CF
                                                                                                                                                         POTENTIAL.
GDNF RECEPTOR ALPHA.
HYDROPHOBIC, REMOVED
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                                                              CRC32;
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HU S., ALTROCK
                                                                                                                                                                                                           SIGNAL.
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D GDNR_MOUSE
D GDNR_MOUSE
AC 99785;
AC P97885;
AC P97885;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN MUSCULUS (MOUSE).
OS MUS MUSCULUS (MOUSE).
TIKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                                                                                           RECEPTOR;
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                                                                                                                                                                        SUBCELLULAR LOCATION: ATTACHED SIMILARITY).
SIMILARITY: BELONGS TO THE GDNF SIMILARITY: BELONGS TO THE GDNF L; AB000800; G1816442; -.
EPTOR; GLYCOPROTEIN; GPI-ANCHOR;
                                                                                                                                                                                                                                                      SIMILARITY).

SUBUNIT: 2 MOLECULES OF GIWITH THE DISULFIDE-LINKED (BY SIMILARITY).
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                                                                                                                           468
 94.5%;
                                                                                                                                                                          GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                       TO THE GDNFR FAMILY
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                                                                                                                                                                                                                                                                    GDNFR-ALPHA ARE THOUGHT TO FORM A ED GDNF DIMER AND WITH 2 MOLECULES
                            POTENTIAL.
POTENTIAL.
6C64C182
                                                                          HYDROPHOBIC,
(POTENTIAL).
POLY-THR.
POTENTIAL.
Score
                                                                                                                                            GDNF RECEPTOR ALPHA.
3183;
                                                                                                                                                                                                                                       TO THE MEMBRANE
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462 463

> 420 420 360 360

240 180 180 120 120 60

300 300 240

CRC32; 80

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Length

REMOVED

DURING

TA BANKS. E GDNF-INDUCED E RET RECEPTOR

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COMPLEX OF RET

BY A GPI-ANCHOR (BY

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                                                                                                                                                                                                                                                                                          GDNR_CHICK

GDNR_CHICK

O13156;

T 01-NOV-1997 (REL. 35, CREATED)

T 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

OT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGI

NTIROTROPHIC FACTOR RECEPTOR 1).
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Matches
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                               CHAIN
PROPEP
                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                      GALLUS GALLUS (CHICKEN)
EUKARYOTA; METAZOA; CHOF
                                           DOMAIN
                                                                                      SIGNAL
                                                                                                                                                                                                                     BUJ-BELLO A., ADU J., PINON L.G., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.; NATURE 387:721-724(1997).
                                                                                SUBCELLE SIMILARITY).

SIMILARITY: BELONGS TO MBL; U90541; G2213803; -
PRCEPTOR; GLYCOPROTEIN; G
27
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
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nes 430; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ш
                                                                                                                                                             SIMILARITY).
SUBUNIT: 2 MOLECULES OF GI
WITH THE DISULFIDE-LINKED
                                                                                                                                            SUBCELLULAR LOCATION: ATTACHED
                                                                                                                                                                                               FUNCTION: RECEPTOR FOR GDNF. MEDIATES AUTOPHOSPHORYLATION AND ACTIVATION OF
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                                                                                                                                                      SIMILARITY)
 361
62
163
346
405
 368
62
163
346
405
                                                                469
                                                                                                                                                                                                                                                                                       CHORDATA; VERTEBRATA;
                                                                                                GPI-ANCHOR; MEMBRANE;
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                                                                                                                                                               OF GDNFR-ALPHA ARE I
                                                                                                                      THE GDNFR FAMILY.
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23; N
                                                     POTENTIAL.
GDNF RECEPTOR ALPHA.
HYDROPHOBIC, REMOVED
(POTENTIAL).
          POTENTIAL.
POTENTIAL.
                                           POLY-THR.
                                                                                                                                                                                                                                                                                                                                  (GDNFR-ALPHA) (TGF-BETA RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . No. 0.00e+00; Mismatches 9;
                                                                                                                                            TO THE
                                                                                                                                                                                                THE
                                                                                                                                            MEMBRANE
                                                                                                                                                                                                                                                                                       TETRAPODA;
                                                                REMOVED
                                                                                                                                                                THOUGHT D WITH 2
                                                                                                                                                                                                GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                   462
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                                                                                                                                                                TO FORM A
                                                                                                                                                                                                                                                                                       AVES; NEOGNATHAE;
                                                                                                                                            ×
                                                                                                                                            GPI-ANCHOR
                                                                MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                OF RET
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Best Local S
Matches 37
    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,

JOHNSON E.M., MILBRANDT J.;

NEURON 18:793-802(1997).

HEURON 18:793-802(1997).

HEURON 18:793-802(1997).

HEURON 18:793-802(1997).

HEURON 18:793-802(1997).

HEURON 18:793-802(1997).

SIMILARITY).

HELDER TO THE CONTER FAMILY

RELEASE TO THE CONTER FAMILY

HELDER TO THE MEMBRANE BY A GPI-ANCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NEURIURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA)
BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BE
                                                                                                          RECEPTOR;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA;
EUTHERIA; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUNER OF TRURZ.
GUNERB OR TRURZ.
MUS MUSCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRTR_MOUSE
                                                                    PROPEP
                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE GDNFR FAMILY. EMBL; AF002701; G2145082; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RODENTIA.
                                                                                                                                                      GLYCOPROTEIN; GPI-ANCHOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469
  52
357
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52
357
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Pred. No. 0.00e+00;
44; Mismatches 43
  TGF-BETA RELATED N
RECEPTOR 2.
HYDROPHOBIC, REMOV
(POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                        MEMBRANE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETRAPODA;
                                                                      REMOVED
                                                                                                               NEUROTROPHIC FACTOR
                                                                                                                                                          SIGNAL
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                                                                      DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAMMALIA;
                                                                                                                                                                                                                                                 GPI-ANCHOR
                                                                        MATURATION
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Best Local (
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                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                             RECEPTOR;
SIGNAL
                                                                                                                       SIMILARITY).
-!- SIMILARITY: BELONGS TY
EMBL; AF002700; G2145080;
                                                                                                                                                         JOHNSON E.M., MILBRANDT J.;

NEURON 18:793-802(1997).

-I- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED

AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.

-I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
          SEQUENCE
                                                              PROPEP
                                                                                                                                                                                                               BALOH R.H., TANSEY M.G., GO HEUCKEROTH R.O., KECK C.L.,
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 97325791.
                                                                                                                                                                                                                                                                                                     (GDNFR-BETA).
GDNFRB OR TRNR2.
                                                                                                                                                                                                                                                                                                                                                                             NRTR_HUMAN 000451;
                                                                                   CHAIN
                                                                                                                    XIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                   382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASFYEFVTSRLSDIFRLASIFSGTGAD::|||||||||||||::::| :
                                                                                                                                                                                                                                                                                                                                                                                                                                            DSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEECEKFLKDFTENPCLRNAIQAFGNGTDVNM-SPKGPTFSATQAPRVE-KTPSLPDDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINCQPESRSVSSCLKENYADCLLAYSGLIGTVMTPNYIDSS-S-LSVAPWCDCSNSGND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFDRV
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                                                                                                       GLYCOPROTEIN;
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357
413
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463
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52
357
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51558 .
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51598
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                                                             464
                                                                                                                                                                                                                                                                               CHORDATA;
                                                                                   ٦
                                                                                                       GPI-ANCHOR;
                                                                                                                                                                                                             GOLDEN J.P., CREEDON D.J.,
L., ZIMONJIC D.B., POPESCU
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                                       RECEPTOR 2.
HYDROPHOBIC, REMOVED I
(POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1522; DB 1;
Pred. No. 0.00e+00;
91; Mismatches 90
      POTENTIAL.
POTENTIAL.
3C74BBFB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
; 0A2165C0 CRC32;
                                                                                 TGF-BETA RELATED NEUROTROPHIC
                                                                                                                                                                                                                                                                               VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                      GDNFR
                                                                                                      MEMBRANE;
                                                                                                                                      FAMILY.
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                                                                                                      SIGNAL
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                                                             DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                               MAMMALIA;
                                                             MATURATION
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                                                                                 FACTOR
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Query Match
Best Local
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Best Local Similarity 48.3%;
Matches 223; Conservative
                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRTR_CHICK STANDARD; PRT; 465 AA. 013157; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPH
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            BUJ-BELLO A., ADU J., PINON L.G., HORTON A., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DI NATURE 387:721-724(1997).
                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALLUS GALLUS
EUKARYOTA; MET
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                                                                                                                                                                                PROPEP
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                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANC
                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLGSYAGMIGFDMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TM---LANK-ECQAALEVLQESPLYDCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLATLYFALPLIDILLSAEVSG-GDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF
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                                                                                                                                                                                                                                                  542; G2213805; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHICKEN).
TAZOA; CHORDATA;
                                                                    8
                                                                                                                 355
387
                                                                                                                                                                                   465
43.98;
                                                                  51908 MW;
                                                                                                                                                                                                                                                     GPI-ANCHOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1522; DB 1;
Pred. No. 0.00e+00;
100; Mismatches 122
Score 1480; DB 1;
Pred. No. 0.00e+00;
                                                               POTENTIAL.
POTENTIAL.
5CA073E4
                                                                                                                                    HYDROPHOBIC, (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                        NEURTURIN RECEPTOR ALPHA.
                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NTNR-ALPHA)
                                                                                                                                                                                                                                                     MEMBRANE;
                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETRAPODA;
                                                                                                                                                                                     REMOVED
                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVIES A.M.
                                                                                                                                                                                                                                                     SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455
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                       Length
                                                                                                                                                                                     DURING
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                                                                                                                                                                                                                                                                                                                                              GPI-ANCHOR
                                                                                                                                                                                     MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEOGNATHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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    P48748;
01-FEB-1996
01-FEB-1996
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                EHV-1 55, VZV 53, EBV BBRF2, HCMV UL103 AND EMBL; X17403; G59711; -
PIR; S09868; S09868.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90269039.

CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R., HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A., PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.CCURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).

-I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                            BRB1_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN UL103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ULA3_HCMVA
                                                                                                                                                                                     178
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                                                                                                                                                                                                                          106 CTVISCVENCULTRKCLHDLLQYLDAVNVRESFGRLLHHSARRLICS 152
                                                                                                                                                                                                                                                                      Local Similarity
mes 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                          CTTSVSNDVCN-RRKCHKALRQFFDKVPAKHSYG-MLFCSCRDIACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEDVNSRLSDIFRVVPFISDVFQQV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRCKRGMRKEIQCLQVYWSIHLGLAEGEEFYEASPYEPITSRLSDIFRLASIFSGM-DPA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNESLASGLEAKDECRSAMEALKQKSLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A-ARILPAVPIVLLKLL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENEIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNTMYDTSIITTCTSIQEHGQKLNKSKEQSLCYSETQLTTDTMPDQKTFVDQKAAGSRHR
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                                                                                                                                                                                                                                                                                                                                                                249 AA;
    (REL.
(REL.
(REL.
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llarity 36.2%;
Conservative
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                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
33, CREATED)
33, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                              28636 MW;
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                                                                                                                                                                                                                                                                    Score 102; DB 1;
Pred. No. 8.87e-03;
8; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
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                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                              239ADB2D CRC32;
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                                                                                              352
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                                                                                                                                                                                                                                                                                                               Length 249
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    RESULT
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DOMAIN
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-!- FUNCTION: THIS IS A RECEPTOR FOR BRADYKININ. COULD CHRONIC PAIN AND INFLAMMATION.
-!- SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORYCTOLAGUS CUNICULUS (RABBIT
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                          SECB_HAEIN STANDARD; PRT; 1
P44853;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UP
01-NOV-1995 (REL. 32, LAST ANNOTATION
    FLEISCHMANN R.D., ADAMS M.D., WHITE O. KERLAVAGE A.R., BULT C.J., TOMB J.-F.,
                                                                                                                                                                                                      PROTEIN-EXPORT PROTEIN SECB OR HI0743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-PROTEIN COUPLED RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U20507; G1041821; PROSITE; PS00237; G_PRO
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-!- INDUCTION: THE R1 RECEDENCE TO COMMISSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACNEIL T., BIERILO K.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                            HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                         STRAIN-RD
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                          PASTEURELLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                MEDLINE; 95350630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                267
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                                                                                                                                                                                                                                                                                                                                                                                                                         CQPESRSVSSCLKENYAD-CL-LA-YSGLIGTVMTPN-YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AILFENCHILA-SLRRRGERVPSRCG-GPRDSKSTALIL-TLVASFLVCWAPYHFFAFLE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLWQVHAIGGCFWEEFTDLGLQLSNFSAFVNSCLNPVIYV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMLFCSCRDIACTERRRQTIVPV-CSYEERE-KPNCLNLQDSCKTNYICRSRLADF-FTN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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352
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larity 26.0%;
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39503
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                                                                                                                                                                                                                               SECB
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                                                                                                                                                              SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 1;
Pred. No. 1.32e-02;
32; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                         169
      DOUGHERTY B.A., MERRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAG_HVIMA STANDARD;
p04594;
13-AUG-1987 (REL. 05, CREATE
01-FEB-1994 (REL. 28, LAST S
01-FEB-1994 (REL. 28, LAST A
GAG POLYPROTEIN (CONTAINS: C
  CHAIN
CHAIN
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CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                      GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

EMBL; K03456; G328021; -

EMBL; X04415; G60229; -

EMBL; A07116; G492872; -

HSSP; P03348; 1HVN.

HIV; K03456; GAGSMAL.
                                                                                                                                                                                                                      AIDS; CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COATON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32758; G1573750; -. TIGR; HI0743; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIZON M., WAIN-HOBSON S., MONTAGNIER CELL 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE) (HIV-1)
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENTIVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS IS ONE OF THE PROTEINS REQUIRED FOR THE NORMAL EXPORT OF ENVELOPE PROTEINS OUT OF THE CELL CYTOPLASM; IT MAY BE INVOLVED IN THE INITIATION OF THE EXPORTING PROCESS, BY BIN TO THE NASCENT POLYPEPTIDE VIA A SIGNAL SEQUENCE, MAINTAINING A STABLE AND PRE-TRANSLOCATION CONFORMATION (BY SHILARITY).

SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORT; TRANSLOCATION.
E 169 AA; 19132 MW; 74BBBAOE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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llarity 25.0%;
Conservative
                                                                                                                                                                                                                                                     POLYPROTEIN;
           56001
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ANNOTATION UPDATE)
CORE PROTEINS P17,
BY SIMILARITY.

MYRISTATE (BY SIMILARITY).

CORE PROTEIN P17 (MATRIX PROTEIN P24 (CORE ANTICORE PROTEIN P2.

CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPS.

CORE PROTEIN P1.

CORE PROTEIN P6.

CORE PROTEIN P6.

CORE PROTEIN P6.
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17; 1
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                  MYRISTYLATION; PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                         PROTEIN P17 (MATRIX PROTEIN).
PROTEIN P24 (CORE ANTIGEN).
PROTEIN P2.
PROTEIN P7 (NUCLEOCAPSID PROTEIN).
PROTEIN P1.
PROTEIN P6.
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2.92e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SONIGO P.;
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Best Local
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                                                                                                                                                                                                                                                                                                         U1-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 80.1 KD PROTEIN IN UME3-PUB1 INTI
YNL021W OR N2819.
                                                                                                                                                                                                                                                                                                                                                                YNC1_YEAST
P53973;
01-OCT-1996
01-OCT-1996
01-OCT-1996
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01-JAN-1990
01-NOV-1997
                                                                                  ANDRE B., IRAQUI HOUSSAINI I., URRESTARAZU L.A., V SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BAN -!- SIMILARITY: BELONGS TO THE RPD3/C08B11.2/ACUC EMBL; 271297; E239664; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 706 AA; 80069 MW; 04B8BCAD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP96_DICDI
P14328;
                                                                                                                                                                                                                                                                           SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN; PHOSPHORYLATION; REPEAT; SPORULATION.

REPEAT 185 197 PRESPORE MOTIF 1.

REPEAT 221 23 PRESPORE MOTIF 2.

REPEAT 298 310 PRESPORE MOTIF 3.

REPEAT 395 407 PRESPORE MOTIF 4.

SEQUENCE 600 AA; 59589 MW; B18FCDB6 CRC32;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X16491; G295736;
PIR; S07638; S07638.
DICTYDB; DD03007; COTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90067962.
FOSNAUGH K., LOOMIS W.F.;
NUCLEIC ACIDS RES. 17:9489-9489(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPORE COAT PROTEIN
                                                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- SUBCELLULAR LOCATION: INTERSPORE MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUMYCETOZOA; DICTYOSTELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 CRNIQCPTGYRCEDHNRNPICVLEERENPDNCLTCNDVNCEASGLVC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 CRDIAC-TE-R-RRQTIVPVCSYEEREKP-NCLNLQD-SCKTN-YIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PHOSPHORYLATED AND FUCOSYLATED. MAY BE MAY CONTAINS GLCNAC-ALPHA-1-P-SER RESIDUES.
SIMILARITY: CONTAINS 4 PRESPORE MOTIFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
19; Conser
Similarity
21; Conser
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2.8%;
ilarity 26.6%;
Conservative
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(REL. 13, LAST SEC
(REL. 35, LAST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%;
larity 41.9%;
Conservative
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LAST ANNOTATION UPDATE)
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PRESPORE MOTIF 2.
PRESPORE MOTIF 3.
PRESPORE MOTIF 4.
W; B18FCDB6 CRC32;
Score 95; DB 1;
Pred. No. 1.38e-01
23; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 93; DB 1;
Pred. No. 2.92e-01
8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
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9.39e-02;
9.39e-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              706
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                                        Length 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 504;
                                                                                                                                                                                     BANKS
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                                                                                                                                                              FAMILY
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Best Local (
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SEQUENCE
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ACT_SITE
METAL
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01-OCT-1996 (REL. 34, LAST SEQUENCE
01-NOV-1997 (REL. 35, LAST ANNOTATI
CELL SURFACE ANTIGEN MS2 PRECURSOR
RICH GLYCOPROTEIN).
ADAMB OR MS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS2_MOUSE
Q05910;
                                                                                                                                                                                                                                                                                                                                                                                                        METALLOPROTEASE); ALSO KNOWN AS THE EMBL; X13335; E264744; -. EMBL; X13335; E225615; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91197896.

YOSHLDA S., SEPOGUCHI M., HIGUCHI Y., AKIZUKI S., YAMAN YOSHLDA S., SEPOGUCHI M., HIGUCHI Y., AKIZUKI S., YAMAN INT. IMMUNOL. 2:585-591(1990).

II FUNCTION: POSSIBLE INVOLVEMENT IN EXTRAVASATION OF C. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

I- TISSUE SPECIFICITY: MACROPHAGES.

I- TISSUE SPECIFICITY: MACROPHAGES.

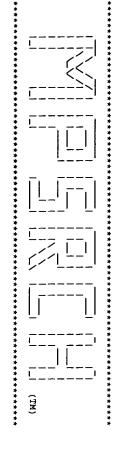
I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC.)
MEDB_GIALA
                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                METALLOPROTEASE;
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00012; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
TRANSMEMBRANE; GLYCOPROTEIN; ANTIGEN; ZINC; HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:107825; ADAM8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ICR;
YAMAMOTO S., YOSHIYAMA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
                                                                        585 ELVLOGTKC-EEGKVC-MDGSCQDLR-VYRSENCSAKCNNHGVCNHKRECH 632
                                                HIPKGNNCLDAAKACNLDDICKKYRSAYITP-CTTSVSND-VCN-RRKCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HITTKSMAAPPSCGLS-PL 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLCIS-NGNYEKEGLGASS 429
                                                                                                  h 2.8%;
Similarity 33.3%;
17; Conservative
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                SIGNAL.
                                                                                                                                                    90046 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SETOGUCHI M.,
                                                                                                   10;
                                                                                                              Score 96; DB 1; Pred. No. 9.39e-02
                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                ZINC (CATALYTIC) (PROBABLE).
BY SIMILARITY.
ZINC (CATALYTIC) (PROBABLE).
ZINC (CATALYTIC) (PROBABLE).
                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                      POTENTIAL.
CELL SURFACE ANTIGEN MS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
 PRT;
                                                                                                                                                    7C26F36F CRC32;
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ION UPDATE)
(EC 3.4.24.-) (MACROPHAGE CYSTEINE-
 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             826 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 REPROLYSIN SUBFAMILY
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                                                                                                   18;
                                                                                                                         Length 826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAMAMOTO S.;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF LEUKOCYTES
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                                                   193
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Matches 1
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J. MOL. BIOL. 231:521-530(1993).
J. MOL. BIOL. 231:521-530(1993).
J. FUNCTION: MAY HAVE A ROLE IN IMMOBILISING THE MICROTUE BETWEEN CELL DIVISIONS.
LIVING SECONDS.
LOCATION: MEDIAN BODY.
LOCATION: MEDIAN BODY.
REPEATING HEPTADS).
EMBL; X64517; G312671; CYTOSKELETON; MICROTUBULES; COILED COIL; HEPTAD REPEAT PAYSEQUENCE 857 AA; 100583 MM; 5EZBBA84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     008014;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MEDIAN BODY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIARDIA LAMBLIA (GIARDIA INTESTINALIS).
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
HEXAMITIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-PORTLAND-1;
MEDLINE; 93287123.
                                                         482 KENSYNFDQLLEQKQQMRSDLNALREKAADYE-RVDRELRLKDKE
                                                                                                                                                                                 7 Match 2.8%;
Local Similarity 33.3%;
nes 15; Conservative
    56 KETNFSLASGLEAKDECRSAMEALKQKSL-YNCRCKRGMK-KEKN
                                                                                                                                                                                 Score 95; DB 1; I
Pred. No. 1.38e-01;
16; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMOBILISING THE MICROTUBULES
                                                                                                                                                                                                                                                                                                                                                                       HEPTAD REPEAT PATTERN CRC32;
                                                                                                                                                                                                                                                                       Length 857
                                                                                                                                                                                          Indels
         98
                                                                                               525
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arch completed: Tue Jun 23 18:20:47 1998 time: 68 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Tue Jun 23 18:21:04 1998; MasPar time 28.26 Seconds 692.865 Million cell updates/sec

ular output not generated.

9:

Title:

Description: Perfect Score: Sequence: >US-08-866-354-2
(1-465) from US08866354.pep
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1 MFLATLYFALPLLDLLLSAE......PLLVLVYTALSTLLSLTETS 465

Scoring table: PAM 150 Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 46.387; Variance 78.836; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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esult No:	Score	Query Match	Length DB	IJ	Description	Pred. No.
٦	3276	97.2	460 2	015507	RET LIGAND 1.	0.00e+00
N	3189	94.7	468 10	035246	GDNF RECEPTOR ALPHA.	0.00e+00
ω	3096	91.9		035252	GDNF RECEPTOR BETA.	0.00e+00
4	3091		463 10	035748	GDNFR-ALPHA/TRNR1-DELT	0.00e+00
رب رب	1525	45.3		035977	GLIAL CELL LINE-DERIVE	0.00e+00
σ	1522	45.2		015316	GLIAL CELL LINE-DERIVE	0.00e+00
7	1522			015328	RET LIGAND 2.	0.00e+00
8	714	21.2	397 10	035118	GFRALPHA-3.	4.75e-136
9	714		397 10	035325	GLIAL CELL LINE-DERIVE	4.75e-136
10	103	3.1	492 11	080624	GAG PROTEIN.	8.13e-02
11	100			Q97845	MATRIX PROTEIN P17 (FR	2.23e-01
12	100		130 11	036786	MA-P17 (FRAGMENT).	2.23e-01
13	100			036808	MA-P17 (FRAGMENT).	2.23e-01
14	100	3.0	133 11	Q97725	MATRIX PROTEIN P17 (FR	2.23e-01
15	100			Q77804	GAG PROTEIN.	2.23e-01
16	86			036772	MA-P17 (FRAGMENT).	4.32e-01
17	99			P89796	GAG PROTEIN (FRAGMENT)	3.11e-01
18	86		1127 3	Q9424B	CODED FOR BY C. ELEGAN	4.32e-01
19	96			P89780	GAG PROTEIN (FRAGMENT)	8.28e-01
20	96		130 11	Q75890	GAG PROTEIN (FRAGMENT)	8.28e-01

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96 2.8 130 11 036773 MA-PIT (FRACMENT) 96 2.8 130 11 075885 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075884 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075888 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075888 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075887 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075844 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075846 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075866 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075867 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075867 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075867 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075868 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075869 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075869 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075869 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075870 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075871 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075873 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075871 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075873 GAG PROTEIN (FRACMENT) 96 2.8 130 11 075871 GAG PROTEIN (FRACMENT) 97 GAG PROTEIN (FRACMENT) 98 130 11 075871 GAG PROTEIN (FRACMENT) 99 10 10 10 10 10 10 10 10 10 10 10 10 10
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Query Match 97.2%; Score 3276; DB 2; Length 460; Best Local Similarity 98.9%; Pred. No. 0.00e+00; Matches 460; Conservative 0; Mismatches 0; Indels 5; Gaps	EMBL; U95847; SEQUENCE 460	EMBL; U97144; G2282026;	RA NAKAGAWARA A.; RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA S.,	RA HISHIKI T KONDOH K. TOHIMIYA S. NIMURA Y. SEKI N. OZAKI T.		SUBMITTED (APR-1997)	PEPINSKY R.B., CATE R.L.;	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R.	RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENPELS C.,		[2]		RA PEPINSKY R.B., CATE R.L.;	WANTED TO DOTTOON G TAMOBEST O WET U TITABLE F., ER	CANTOOLA W UPSCION CA WODIEV D S CARMILLO D FURFACELS		[1]	EUTHERIA: PRIMATES.	EUKARYOTA: ME	ON RETUL.	RET LIGAND 1	01-JAN-1998 (TREMBLREL. 05, LAST	01-JAN-1998 (TREMBLREL. 05,	01-JAN-1998 (TREMBLREL		RESULT 1
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035246;
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01-JAN-1998
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DEY B.K., WONG Y.W., TOO H.P.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF014117; G2624961; -.
SEQUENCE 468 AA; 51752 MW; AFDCE6A1 CRC32;
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STRAIN-C57; TISSUE
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STRAIN-C57; TISSUE-LIVER;
DEY B.K., WONG Y.W., TOO
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l Similarity 93.1%;
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Pred. No. 0.00e+00;
23; Mismatches 8
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ANNOTATION UPDATE)
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SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL, AF015172; G2624963; -.
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;
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O1-JAN-1998 (TREMBLREL 0)
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O1-JAN-1998 (TREMBLEEL 0)
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GDNFR-BETA OR RETL2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORD.
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;
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    SEQUENCE FROM
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425; Conser
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larity 91.8%;
Conservative
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                                                                   CHORDATA;
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05, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDAT
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                                                                                                                                   NEUROTROPHIC
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i, LAST SEQUENCE UPDATE)

5, LAST ANNOTATION UPDATE

7. TREOPHIC FACTOR RECEPT
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Pred.
27; M
                                                                   VERTEBRATA;
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No. 0.00e+00;
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SANICOLA M., HESSION C.A.,
WALUS L., ROBINSON S., JAWG
PEPINSKY R.B., CATE R.L.;
PROC. NATL. ACAD. SCI. U.S.
                                                                                              015316 PRELIMINAR
015316; TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
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PEPINSKY R.B., CATE R.L.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF005226; G2232252; -.
EMBL; U97143; G2282024; -.
SEQUENCE 464 AA; 51668 MW; B1A2BD11 CR
SEQUENCE FROM N.A.
TISSUE-FETAL BRAIN;
WARTIOVAARA K., SUVANTO P.,
MOSHNYAKOV M., AIRAKSINEN M.
                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BRAIN/KIDNEY;
SANICOLA M., HESSION C.A.,
                                                                                       GDNFR-BETA
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209; Conservative
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D NEUROTROPHIC
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EMBL/GENBANK/DDBJ
                                                                                       , CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE
, LAST ANNOTATION RECEPT
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HORELLI-KUITUNEN N., S., PALOTIE A., SARI
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Pred. No. 0.00e+00;
93; Mismatches 106;
                                                                                                                                                      PRT;
                                                                 VERTEBRATA;
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I H., TIZARD
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H., TIZARD
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                                                                  TETRAPODA;
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  SARIOLA
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                                                                  MAMMALIA;
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O15328;
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O1-JAN-1998
O1-JAN-1998
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                                            SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R. PEPINSKY R.B., CATE R.L.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U97145; G2282028; -.
SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;
                                                                                                                                                           WALUS L., ROBINSON C.A., WORLEY D. WALUS L., ROBINSON S., JAWORSKI G., PEPINSKY R.B., CATE R.L.,
PROC. NATL. ACAD. SCI. U.S.A. 94:623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; U93703; G2228737; -. SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;
                                                                                                                                                                                                                                                           EUKARYOTA;
                                                                                                                        TISSUE-LIVER;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                              417
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                                                                                                                                                                                                           SSUE-LIVER;
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           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                     SAPIENS (HUMAN).
SAPIENS (HUMAN).
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. Similarity 48.3%, 223; Conservative
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Similarity 48.3%;
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          45.2%;
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; Pred. No. 0.00e+00;
100; Mismatches 122; Indels 17;
Score 1522; DB 2;
Pred. No. 0.00e+00;
100; Mismatches 122;
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RESULT 8
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DT 01-JAN-1998
DT 01-JAN-1998
DE GFRALPHA-3
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GN GFRALPHA-3
OS MUS MUSCULUS
OC EUTHERIA; ROI
RN [1]
RP SEQUENCE FROM
RC STRAIN-C57BLG
RA NOMOTO S. IT
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SQ SEQUENCE 30
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S EUKARYOTA; METAZOA; CHORDATA; VI
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Best Local S
Matches 12
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STRAIN-C57BL6; TISSUE-HEART;
NOMOTO S., ITO S., YANG L., ADACHI K., KIU
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ
EMBL; AB008833; D1024441; -
SEQUENCE 397 AA; 44307 MW; A80E0D24 CF
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FLATLYFALPL-LDLLLSAEVSGGDRL-D-CVKASDQCLKEQSCSTKYRTLRQCVAGKET
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                        CTTSVSNDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC-R-DIACTERRRQTIVPVCSY
                                                CS-GIR----CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL
                                                                          DSPYEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITP
                                                                                                VSPYE - - DTVTSKPWKM - N - LSKL - NMLK - - PDSDLCLKFAMLCTLHDKCDRLRKAYGEA
                                                                                                                           NFSLASGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQ-GNDLLE
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LAST ANNOTATION UPDATE)
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Pred. No. 4.75e-136;
70; Mismatches 135;
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01-JAN-1998 (TREMBLREL 0
01-JAN-1998 (TREMBLREL 0
01-JAN-1998 (TREMBLREL 0
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01-NOV-1996
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STRAIN-VI205; TISSUE-BLOOD;
LOUWAGIE J.J., MCCUTCHAN F., BRENNAN T., P
SANDERS-BUELL E., EDDY G., DER GROEN G., F
GERSHY-DAMET M., DELEYS R., BURKE D.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF020305; G2429367; -.
SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;
                                                                                                 HUMAN IMMUNODEFICIENCY VIRUS TYPE VIRIDAE; SS-RNA ENVELOPED VIRUSES;
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                                                                                       LENTIVIRINAE
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1 Similarity 35.2%;
123; Conservation
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Pred. No. 4.75e-136;
70; Mismatches 135;
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Best Local S
Matches 1
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Q97845;

Q97845;

Q1-FEB-1997 (TREMBLREL. 02, LAST

P 01-FEB-1997 (TREMBLREL. 02, LAST

T 01-FEB-1997 (TREMBLREL. 02, LAST

O1-FEB-1997 (FREMBLREL. 02, LAST

PROTEIN P17 (FRAGMENT).
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Best Local S
Matches 1
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O36786; O1-JAN-1998 (TREMBLREL. C
01-JAN-1998 (TREMBLREL. C
01-JAN-1998 (TREMBLREL. C
                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
LEIGH BROWN A.J., LOBIDEL D., WADE
BRETTLE R.P., FRANCE A.J., LEEN C.S
BRETTLE R.P., FRANCE A.J., ROBERTSON J.I
                                                                                       NON_TER
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EMBL; X99948; E258593; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L11785; G555036; -. SEQUENCE 492 AA; 54981 MW;
                                                                                SEQUENCE
                                                                                                         MAW R.D., MULCAHY F., ROBERT: PEUTHERER J.F.; VIROLOGY 235:166-177(1997). EMBL; AF014183; G2406708; -.
                                                                                                                                                                                                    HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND;
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LENTIVIRINAE.
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VIRIDAE; SS-RNA ENVELOPED VIRUSES; F
                                                                                                                                                                                          LENTIVIRINAE
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(FRAGMENT).
                                      h 3.0%;
Similarity 41.9%;
18; Conservative
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Similarity 41.9%;
18; Conservative
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Similarity 42.5%;
17; Conservative
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130 AA;
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129 AA;
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14550 MW;
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14584 MW;
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Pred. No. 2.23e-01;
11; Mismatches 9;
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Pred. No. 8.13e-02;
9; Mismatches 10
                                      Score 100; DB 11; 1
Pred. No. 2.23e-01;
11; Mismatches 9;
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.S., MCMENAMIN
.R., SANKAR K.N
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POSITIVE-STRAND;
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DT OG

DT OG

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AC Q7
D7 Q7
D7 Q1
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Best Local Similarity 44.2%;
Matches 19; Conservative
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                                                                                                   077804
077804;
01-NOV-1996
01-NOV-1996
01-NOV-1996
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Q97725
Q97725;
GAG PROTEIN.
HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATRIX PROTEIN.
NON_TER 133
SEQUENCE 133 AA;
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EMBL: Z79562; E261908; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
MATRIX PROTEIN P17 (FRAGMENT).
HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
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LEIGH BROWN A.J., LOBIDEL D., WADE C.M., REBUS S., PHILLIPS N.,

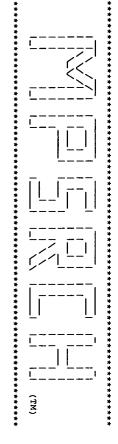
BRETTLE R.P., FRANCE A.J., LEEN C.S., MCMENAMIN J., MCMILLAN A.,

MAW.R.D., MULCAHY F., ROBERTSON J.R., SANKAR K.N., SCOTT G., WYLD R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
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EMBL; AF014205; G2406752; -.
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                                                                                                                                                                                                                                                                                                           28 KYR-LKHIVWASRELERFALNPGLLEASEGCRQILGQL-QPSL 68
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Local Similarity 39.5%;
les 17; Conservative
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130 AA; 14527 MW; 7325723C CRC32;
                                                                                                 (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
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14724 MW;
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05, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
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Pred. No. 2.23e-01;
9; Mismatches 10
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Pred. No. 2.23e-01;
12; Mismatches 9
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                                                                                                    Query Match 3.0%;
Best Local Similarity 32.9%;
Matches 24; Conservative
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STRAIN-DJ258; TISSUE-BLOOD;
LOUWAGIE J J., MCCUTCHAN F., BRENNAN T., PEETERS M.,
SANDERS-BUELL E., EDDY G., DER GROEN G., FRANSEN K.,
GERSHY-DAMET M., DELEYS R., BURKE D.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L11763; G554842; -.
SEQUENCE 486 AA; 54094 MM; 6CB6088C CRC32;
                                                                                                                                                                                                                                                                           LENTIVIRINAE
 102 IYWSMYQSLQGND
                         84 VLWCVHQRIDIKD 96
                                                 Score 100; DB 11;
Pred. No. 2.23e-01;
18; Mismatches 24
                                                                                                                              Length 486;
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                                                                                                                                                                                                                        BRENNAN
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                                                                                                    Gaps
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Search completed: Tue Jun 23 18:23:21 1998 Job time : 137 secs.



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

9.. ular output not generated. Wed Jun 24 20:41:51 1998; MasPar time 2627.46 Seconds 1357.834 Million cell updates/sec

Title: >US-08-866-354-3 (1-2138) from US08866354.seq 2138

Description:
Perfect Score:
N.A. Sequence:
Comp: Scoring table: TABLE default Gap 6 1 AGCTCGCTCTCCCGGGGCAG......AGACAGGCCCGCAGCCGTCG 2138
TCGAGCGAGAGGGCCCCGTC.....TCTGTCCGGGCGTCGGCAGC

Nmatch STD : Dbase 0; Query 0

Searched:

457396 segs, 834342348 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

genbank106
13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat
19:gb_ph 20:gb_pl 21:gb_pr1 22:gb_pr2 23:gb_ro 24:gb_st
25:gb_sy 26:gb_un 27:gb_v1 1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_vi

tatistics: Mean 11.685; Variance 5.512; scale 2.120

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	58.2 2560 22 AF038421 53.3 1619 22 AF042080 52.8 2175 22 HSU95847 51.1 1707 22 HSU97144 29.9 777 23 AF012811 27.0 3037 17 GG990541 12.9 596 22 HSGFRA1G06 11.4 497 22 HSGFRA1G03	Result NO. 1 2 3 4 6	Score 2138 2081 1615 1379 1302	Query Match 100.0 97.3 75.5 64.5 60.9	Length 2138 3616 2549 1651 1392	388888	ID 	Description Rattus norvegicus G Rattus norvegicus R Mus musculus GDNF r Mus musculus GDNF r Mus musculus GDNF r Mus musculus GDNF r	DNF
58.2 2560 22 AF038421	53.3 1619 22 AF042080 52.8 2175 22 HSU95847 51.1 1707 22 HSU97144 29.9 777 23 AF012811 27.0 3037 17 GG990541 12.9 596 22 HSGFRA1G06 11.4 497 22 HSGFRA1G03	Sc. 22	138 138 1515 1515 179 1879 1879 1879	Match 100.0 97.3 75.5 64.5 60.9 59.8	Length 2138 3616 2549 1651 1392 1415 2560	2233223 B	RNU59486 RNU97142 AF014117 AF015172 AB000800 AF038421	Description Rattus nor Rattus nor Mus muscull Mus muscull Rattus nor Mouse mRNA Homo sapie	Description Rattus norvegicus GDNF Rattus norvegicus RET Mus musculus GDNF rece Mus musculus GDNF rece Mus musculus GDNF rece Mattus norvegicus mRNA Mouse mRNA for GDNF re HOMO sapiens GPI-linke
	52.8 2175 22 HSU95847 51.1 1707 22 HSU97144 29.9 777 23 AF012811 27.0 3037 17 GGU90541 12.9 596 22 HSGFRA1G06 11.4 497 22 HSGFRA1G03		1139	53.3	1619	22	AF042080	Homo sapie	Homo sapiens glial cel
53.3 1619 22 AF042080	51.1 1707 22 HSU97144 29.9 777 23 AF012811 27.0 3037 17 GGU90541 12.9 596 22 HSGFRA1G05 11.4 497 22 HSGFRA1G03		1128	52.8	2175	22	HSU95847	Human GDNI	Human GDNF receptor al
53.3 1619 22 AF042080 52.8 2175 22 HSU95847	29.9 777 23 AF012811 0 27.0 3037 17 GG990541 1 12.9 596 22 HSGFRA1G06 1 11.4 497 22 HSGFRA1G03		1093	51.1	1707	22	HSU97144	Homo sapi	Homo sapiens RET ligan
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ALIGNMENTS

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/coon_start=1 /product="GDNF_receptor alpha" /product="GDNF_receptor alpha" /db_xref="PID:g1399863" /translation="MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST_/translation="MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST_KYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRI KYMYQSLOGNDLLEDSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKA QNLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRD IACTERRRQTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFFINCQPESRSVSN CLKENYADCLLAYSGLIGTVMTPNYVDSSSLSVAPMCDCSNSGNDLEDCLKFLNFFKD	/organism="kattus norvegicus" /db_xrefe"taxon:10116" 302.:1708	Location/Qualifiers	Direct Submission Submitted (29-MAY-1996) Immunology, Amgen, Inc., Amgen Center, Thousand Oaks, CA 91320-1789, USA	Fox,G.M., Jing,S.J., Yu,Y., Holst,P.L., Fang,M., Tamir,R., Antonio,L., Hu,Z. and Louis,JC.		mediated by GDNFR-alpha, a novel receptor for GDNF Cell 85 (7), 1113-1124 (1996)	Fox, G.M. GDNF-induced activation of the ret protein tyrosine kinase is	<pre>Murinae; Rattus. 1 (bases 1 to 2138) 1 (chases 1 to 2138) Jing,S.J., Wen,D., Yu,Y., Holst,P.L., Luo,Y., Fang,M., Tamir,R., Antonio,L., Hu,Z., Cupples,R., Louis,JC., Hu,S., Altrock,B. and</pre>	Norway rat. Rattus norvegicus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;	52	RNU59486 2138 bp mRNA ROD 23-JUL-1996

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Center, Cambridge, MA 02142, USA
Location/Qualifiers
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Submitted (15-JUL-1997) Blochemistry,
Singapore 119260, Singapore
Location/Qualifiers
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2 (bases 1 to 2549)
Dey,B.K., Wong,Y.W. and T
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Dey,B.K., Wong,Y.W. and Too,H.P.
Cloning of a novel murine isoform
neurotrophic factor receptor
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//translation="MFLATLYFVLPLLDLLMSAEVSGDRLDCVKASDQCLKEQSCST
//translation="MFLATLYFVLPLLDLLMSAEVSGDRLDCVKASDQCLKEQSCST
KYRTLRQCVAGKETNYSLTSGLEAKDECRSAMEALKQKSLYNCRCKCRGMKKEKNCLRI
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CNLDDTCKKYRSAYITPCTTSMSUNEVCHNKALRQFFDKVPAKHSYGNLFCSCRD
VACTERRRQTIVPVCSYEERERPNCLMLQDSCKTNYICRSRLADFFTNCQPESRSYSN
CLKENYADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKD
NTCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRIKNKPLGPAGSENEIPTHVL
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Dey, B.K., Wong, Y.W. and Too, H.P. Direct Submission
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RRRQTIVPVGSYEERERPNCLMQDSCKTATVYICRSKLADFFTNCQPESREVSNLKEN
YADCLLAYGLLGTVMTPNYIDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLK
NAIQAFGNGSDYTMWQPAPPVQTTTATTTAFRIKNKPLGPAGSENEIFHVLPPCAN
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Query Match
Best Local Similarity
Matches 1549; Conser

64.5%; llarity 94.2%; Conservative

Score 1379; DB 23; Pred. No. 0.00e+00; 0; Mismatches 80;

Length 1651; Indels

15;

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                             TGAAGTCTGCAACCGCCGCAAAGTGCCACAAAGCCCTCAGGCAGTTCTTCGACAAAGTTCC
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complete cds.
AJ002072
92564301
GDNFR-alpha/TrnR1-delta F
                                                                                                                                                                            Direct Submission
Submitted (16-OCT-1997) Zhong J.,
NC7/172, Ruhr University Bochum,
                                                                                                                                             Zhong, J., Annies, M.
                                                                                                                                                                                                             Zhong, J
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                                                                                                                                                                                                                                             Eukaryotae; Metazoa;
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Lished
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/codon_start=1
/product="GDNFR-alpha/TrnR1-delta protein"
/db_xref="PID:e1154274"
/db_xref="PID:e2564302"
/translation="MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCST
                                                                /organism="Rattus norvegicus"
/strain="Hannover"
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GDNFR-alpha,
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hi; Muridae; Murinae; 1
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AACTACGCAGACTGCCTCCTGGCCTACTCGGGGACTGATTGGCACAGTCATGACTCCCAAC
                                               TGCACCGAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAGG
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YGSMYGSLQGNDLLEDSPYEEVNSRLSDIFRAVPFIVEHISKGNNCLDAAKACNLDD
TCKKYRSAYITDCTTSMSNEVCURRKCHKALROFFBYSTNCHSYGMLFCSCRDJACTE
RRRQTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKEN
YADCLLAYSGLIGTVMTPNYVDSSSLSVAPWCDCSNGSNDLEDCLKFLNFFKNNTCLK
NAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCAN
LQAQKLKSNYSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMTTA
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0; Mismatches 0;
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Mouse mRNA
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Direct Submission

Submitted (30-JAN-1997) to the DDBJ/EMBL/GenBank databases.

Kazuhiko Watabe, Tokyo Metropolitan Institute for Neuroscience Neuropathology; Musashidai 2-6, Fuchu, Tokyo 183, Japan (E-mail:kazwtb@tmin.ac.jp, Tei:0423-25-3881, Fax:0423-21-8678)

1. 1415
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
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RESULT 7
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Angrist,M., Jing,S., Bolk,S., Bentley,K., Nallasan Halushka,M., Fox,G.M. and Chakravarti,A.

Human GrRAH: Cloning, mapping, genomic structure, a candidate gene for Hirschsprung disease suscepti Genomics 48, 354-362 (1998)

2 (bases 1 to 2560)

Angrist,M., Jing,S., Bolk,S., Bentley,K., Nallasan Halushka,M., Fox,G.M. and Chakravarti,A.

Direct Submission
Direct Submission
Cleveland, OH 44106-4955, USA Homo sapiens AF038421 g2921531 Eukaryota; Metazoa; Chordata; Ve. Primates; Catarrhini; Hominidae; Homo sapiens AF038421 human /chromosome="10" /map="10q25" /organism="Homo sapiens" /db_xref="taxon:9606" 2560 bp | GPI-linked | mRNA PRI 10-APR-1998 anchor protein (GFRA1) mRNA, complete Vertebrata; Mammalia; Ното. structure, and evaluation ase susceptibility Nallasamy Nallasamy,S 10-APR-1998 Eutheria 2109 cds 25

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                                                                       GAGGATTCCCCATATGAACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCA
                                                                                                          AAGAACTGCCTGCGCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTG
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     TTCATATCAGATGTTTTCCAGCAAGTGGAACACTTTCCAAAGGGAACAACTGCCTGGAC
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larity 84.9%;
Conservative
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//gene="GFRA1"
//note="similar to GDNE Receptor alpha; part of functional
//note="similar to GDNE Receptor kinase"
//docon_start=1
//codon_start=1
//product="GPI-linked anchor protein"
//db_xref="prD:g2921532"
//translation="MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
KYRTLRQCVAGKETNFSLASGLEAKDECKSAMEALKQKSLYNCRCKRGMKKEKNCLRI
YWSMYOSLOGNDLLEDSEYEPVNSRLSDIFRVVPPISDVFQQVEHIPKGNNCLDAKA
CNLDDICKKYRSAYITPCTTSVSNDVCNRRKCHKALRQFFDKVPAKHSYGNLFCSCRD
IACTERRQTIYVPCSYEEREKENCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSS
CLKENYADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNSGNDLEECLKFLNFFKD
NTCLKNALQAFGNGSDVTVWQPAFPQTTTATTTTALRVNKFLGPAGSENEIPTHYL
PPCANLQAQKLKSNVGGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSCGLSPLLVL
VVTALSTLLSLTETS"
42 a 675 c 632 g 611 t
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1. No. 0.00e+00;
Mismatches 272;
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JOURNAL REFERENCE
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Best Local Similarity
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alpha (GFRA1) I
AF042080
g2801556
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2 (bases 1 to 1619)
Shefelbine, S. E., Khorana, S.,
Hu, Z. J., Fox, G.M., Jing, S., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JAN-1998) Endocrinology-Box 15, M.D. Center, 1515 Holcombe Blvd, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shefelbine, S.E., Khorana, S., Schultz, P.N., Huang, E., Hu, Z.J., Fox, G.M., Jing, S., Cote, G.J. and Gagel, R.F. Mutational analysis of the GDNF/RET-GDNFRa signaling kindred with vesicoureteral reflux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1619)
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                                                                                                                                                                             409
                                                                                            53.3%;
llarity 86.5%;
Conservative
                                                                                                                                                                                                                                                                 '/product-"glial cell line-derived neurotrophic factor receptor alpha"

/db_xref-"pID: 92801557"

/translation-"MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
/translation-"MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
/translation-"MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
/translation-"MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKEQSCST
/translation-"MFLATLYFALPLLDLLCSAMEALKQXSLYLCCKCKGKKKKNCLRA
/TRANSUSLAGNULLEDSSYEPWSTUTALTYFALFYWAYATSTALTYTCAFTLAFT
LACTERRACTIVPVCSYEFEKENCLNLQDSCKTNYICRSRLADFTNCQPESSRSVSS
CLKENYADCLAYSGLIGTVMTPNYIDSSSLYAPWCDCSNGGNDLEECLKFLNFFKD
NTCLKNALQAFGNGSDVTVMQPAFPQOTTTATTTTALRYKNKPLGPAGSGNEIFTHYL
PPCANLQAQKLKSNYSGNTHLCISNGNYEKEGLGASSHITTKSMAAPPSCGLSPLLVL
LYVTALTTI CTTTST"
                                                                                                                                                                      /gene="GFRA1"
/note="found to be alternative
of genomic sequence"
a 448 c 419 g 343 t
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                                                                                                                                                                                                                                                       VVTALSTLLSLTETS"
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111. .1508
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/note="GPI-linked receptor"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"GDNFRa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type="medullary thyroid carcinoma.
                                                                                          Score 1139; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 211;
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Gagel,R.F.
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Primates; Catarrhini; Hominidae; Homo.
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GDNF-induced differentiation and its enhancement by retinoic acid in primary human neuroblastomas expressing c-Ret and GDNFR-alpha
                                                                                                                                                                                  Submitted (31-MAR-1997) Division of Biochemistry, Chiba Cancer Center Research Institute, 666-2, Nitona, Chuoh-ku, Chiba 260,
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Direct Submission
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                                                                                                         AAAGCTTGT-G-GC-CCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGCTAATTCCAAA
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CGCCGGCACCATGITCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCT
                                                                                                                                                     GAGCTGAACTTTGGGCGGCCAGAACAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCT
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                                                      GAGCTGAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGGATCGCTGCACGCTGAGCT
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/db_xref="taxon:9606"
/dev_stage="embryonic"
/tlssue_type="kidney"
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/db_xref="pid:g2282026"
/db_xref="pid:g2282026"
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/translation="mflatlyFalplldllsaevSggDrldcvkaSDoclkeOSCST
KYRTLRQCVAGKETNESLASGLEAKOECRSAMEALKOKSLYNCRCKRRMKKEKNCLRI
YMSMYOSLQGNDLLEDSPYEPVNSRLSDIFRVVPFISVEHIPKGNNCLDAAKACNLDD
ICKKYRSAYITPCTTSVSNUVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTE
RRRQTIVPVCSYEEREKPNCLNLQDSCKTNYICRSRLADFTNCQPESESVSSCLKEN
YADCLLAYSGLIGTVMTPNYIDSSSLSVAPWCDCSNGSNDLEECLKFLNFFKONTCLK
NAIQAFGNGSDVTVMQPAFPVQTTTATTTTALRYKNKPLGPAGSENEIPTHVLPPCAN
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GACCCCCAACTACATAGACTCCAGTAGCCTCAGTGTGGCCCCCATGGTGTGACTGCAGCAA 1196
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Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                  735;
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Submitted (08-JUL-1997) Laboratorio
Istituto Glannina Gaslini, Largo G.
Location/Qualifiers
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Puliti, A. and Seri, M.
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larity 93.6%;
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/db_xref="pID:g2286225"

/translation="LNuQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLL
/translation="LNuQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLL
AYSGLIGTVMTPNYIDSSLSVAPWCDCSNSCNDLEDCLKFLMFFKDNTCLKNAIQAF
GNGSDVTMWQDAAPPVQTTTATTTTAFRIKNKPLGPAGSENEIPTHVLPPCANLQAQKL
KSNVSGSTHLCLSDNDYGKDGLAGASSHITTKSMAAPPSCGLSSLPVMVFTALAALLS
                                                                                                                                                                                                                                                                                             from Soares
Consortium"
                                                                                                                                                                                                                                                                                                                         /clone="402011"
                                                                                                                                                                                                                                                                                                        /note="EST deposited under GenBank Accession Number W76716
from Soares mouse embryo NbME13.5 14.5 cDNA library; IMAGE
                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
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g2213802
                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 3037)

Buj-Bello,A., Adu,J., Pinon,L.G., Horton,A., Thompson,J. Rosenthal,A., Chinchetru,M., BuChman,V.L. and Davies,A.M. Neurturin responsiveness requires a GPI-linked receptor receptor tyrosine kinase Nature 387 (6634), 721-724 (1997)
                                                                           Nature 30
97336104
2 (base
Direct Submission
Submitted (24-FEB-1997) Biol. Med. Sciences, Univ. of
Bute Medical Buildings, St. Andrews, Fife KY16 9TS, Sc
Location/Qualifiers
1. .3037
                                                             2 (bases 1 to 3037)
Buchman, V.L.
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                                                  GAAAGGAGGCGGCAGACTATTGTTCCTGTGTGTTCATATGAGGACAGGGAGAAACCAAAC 1462
                                     GAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGGGCCCAAC
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larity 78.1%;
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CSTKYRPTRQCVAGKESNETSRATGLBAKDECKSAMEALKQKSLYNGRCKRGMKKEKNC
LRIWSMYQSLOGNDLLEDSPYEDVNSRLSDIFTRLAPIVSVEPVLSKGNNCLDAKAG
NLNDTCKRFRSAYITPCTSSTSNEICNKRKCHKALRLEFDKVPPKHSYGMLFCSCRDV
ACTERRROTIVPVCSYEDREKPNCLNLQESCKKNYLORSRLADFTNCQPESRSVSSC
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TCLKNALQAGEGGTDVWVQPFLLPVOTTTATTTASEKLKNTGSETTNNEIPFHNDSPA
CANLQAQKKRKSNESVDTELCLNENAIGKDNTPGVSTSHISSENSFALPTSFYPSTPL
ILMTLASLFLESSSVVL"
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/db_xref="taxon:9031"
740. .2150
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740. .2149
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/note="GPI-linked component of GDNF
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                                                                                                                                                                                          Angrist, M., Jing S., Bolk, S., Bentley, K., Na Halushka, M., Fox, G.M. and Chakravartt, A. Human GFRA1: Cloning, mapping, genomic struc a candidate gene for Hirschsprung disease su Genomics 48, 354-362 (1998)

2 (bases 1 to 596)
Angrist, M., Jing, S., Bolk, S., Bentley, K., Na Halushka, M., Fox, G.M. and Chakravarti, A.
                                                                                                                                                                                                                                                                                                                                                                                                     N Homo sapiens GPI-linked a;
AF038415
g2921538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCAAGTAGTCTCAGCGTTGCCCCCATGGTGTGACTGCAGCAACAGTGGTAATGACATA 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGACTGCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAACTACGTA 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGACTGCCTCCCTCGCTTACTCGGGGCTCATTGGCACAGTGATGACACACGAACTACATA 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTCACAAACTGCCAGCCTGAGTCACGCTCTGTTAGTAGCTGTCTGAAGGAGAACTAC 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGACTGCTTGAAATTTCTGAATTTTTTTAAGGACAATACTTGTCTCAAAAATGCAATT 1327
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                                                                                                                                                                Direct Submission Submitted (12-DEC-1997) Genetics,
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.
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              152
                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q25"
147. 483
/gene="GFRA1"
              /number=6
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              163
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protein (GFRA1) gene, exon
              125
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GAATTTGCAGGACTCCTGCAAGACGAATTACATCTGCAG 483
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                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)

Angrist, M., Jing, S., Bolk, S., Bentley, K., Nallasamy, S.,

Halushka, M., Fox, G.M. and Chakravarri, A.

Human GPRA1: Cloning, mapping, genomic structure, and evaluation
a candidate gene for Hirschsprung disease susceptibility
Genomics 48, 354-362 (1998)

2 (bases 1 to 497)

Angrist, M., Fox, G.M. and Chakravarri, A.

Direct Submission

Direct Submission
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Homo sapiens
AF038412
                                               . Similarity
270; Consei
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                                               11.4%;
larity 91.2%;
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larity 90.6%;
Conservative
                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q25"
76. 369
                                                                                                            /number-3
                                                                                                                                 /gene="GFRA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 bp
GPI-linked
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                                             Score 244; DB 22;
Pred. No. 2.41e-178;
0; Mismatches 26;
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Pred. No. 1.19e-205;
0; Mismatches 32;
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anchor
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                                                                      Length 497;
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1. 1395
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning, mRNA distribution and chromosomal localisation of the gene for the human glial cell line-derived neurotrophic factor beta, a homologue to GDNFR-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wartiovaara K., Suvanto P., Horelli-Kuitunen N.,
Moshnyakov M., Alraksinen M.S., Palotie A., Sario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GDNFR-beta) mRNA,
U93703
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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727-APR-1998 (first entry)
Rat glial cell derived neurotrophic factor receptor alpha; cDNA.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; rat; kidney disease; glomerulonephritis; therapy; ds. mat_peptide sig_peptide Location/Qualiflers 117..1523 /*tag* a 117..188 /*tag* b 189..1520 /*tag* c

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cc relates to novel uses of GDNF and its receptor. In particular, it cc relates to native rat GDNFF alpha (see W27327), its variants and cc soluble derivatives (extracellular domain), chimeric GDNFF alpha (cc and antibodies which bind to the GDNFF alpha, including agonist cc and neutralising antibodies, as well as various uses for these cc molecules. It also relates to assay systems for detecting ligands ct to GDNFF alpha, systems for studying the physiological role of cc GDNFF diagnostic techniques for identifying GDNF-related conditions, cc methods for identifying molecules homologous to GDNFF alpha, and cc therapeutic techniques (claimed) for the treatment of GDNF-related conditions, particularly kidney disease cassociated with glomerulonephritis and enteric nervous system cc claimed disorders. Transgenic and knockout animals are allowed.
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                  ctggacgacacctgtaagaagtacaggtcggcctacatcacccccttgcaccaccaccagcatt
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GAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAGGCCCCAAC
                                                                                                                                        TCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTTCGACAAG
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Pred. No. 0.00e+00;
0; Mismatches 1;
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ttgccttctgaagacaggccgcagcc 1949	TACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGTCTTACTCAGCAGCA 2107	actggttaggaacaggagatactattgataaagattcttccatgtcttactcagcagc	TTTAACAGCTTGAACCCTGTTCTC	ggtgaggatggtggtggtgatgatggtgattttaacagcttgaaccctgttctct	gtgcggcttaaggggaccattgcaccatgtaaagcaagctgggcttatcatgtgtttga 1802	A STANDARM TO THE TENT TO THE TENT TO THE TRANSPORT OF THE TOTAL TOTAL TO THE TOTAL	gggcttctgttgaagaactgctacagggctaattccaaaacccataaggctctgggggcgtg 1742 	GCAGTTTCACCCAACTGGAACTCTTTCCTTGTTTTTAAGAAAGCTTGTGGCCCTCA	aagcagttto	CAAGTATTCTGTCCCTGTCCTCTTGTATATCTGAAAATCCAGTTTTAAAAGCTCCGTTGA 1807	aagtattotgtoootgtootottgtatatotgaaaatocagttttaaaagotoogttg		cgttggcagaaacgtcgtagctgcatccgggaaaacagtatgaaaagacaaaagac		gcagtctgagctcactgccggtgctgatgctcaccgcccttgctgccctgttatctgt	GATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAATCAATGGCTGCTCCTCCCAGC 1627	atggtctcgctggtgcctccagccacataaccacaaaatcaatggctgctcctcccagc 14	CTGAAATCCAATGTGTCGGGTAGCACACACCTCTGTCTTTCTGATAGTGATTTCGGAAAG 1567	tgaaatccaatgtgtcgggtagcacacctctgtctttctgatagtgatttcggaaag 13	TCTGAGAATGAGATCCCCACACACGTTTTACCACCCTGTGCGAATTTGCAGGCTCAGAAG 1507	ctyagaatgagatccccacacacgttttaccaccctgtgcgaatttgcaggctcagaag 13	ACCACTGCCACCACCACCACCTGCCTTCCGGGTCAAGAACAAGCCTCTGGGGCCCAGCAGGG 1447	ccactgccaccactaccactgccttccgggtcaagaacaagcctctggggccagcaggg 1	CAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGC	aagcetttggcaatggetcagatgtgaceatgtggcagecageeetecagtecag	GAAGACTGCTTGAAATTTCTGAATTTTTTTAAGGACAATACTTGTCTCAAAAATGCAATT 1327	aagactgcttgaaatttctgaatttttttaaggacaatacttgtctcaaaaatgcaatt 11	GACTCCAGCAGCCTCAGCGTGGCACCATGGTGTGACTGCAGCAACAGCGGCAATGACCTG 1267	actccagcagcctcagcgtggcaccatggtgtgactgcagcaacagcggcaatgacctg 1	GCAGACTGCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAACTACGTA 1207	cagactgcctcctggcctactcgggactgattggcacagtcatgactcccaactacgt	TITITACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGAGAACTAC 1147	tttttaccaactgccagccagagtcaaggtctgtcagcaactgtcttaaggagaactac 9	GCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCTTGCAGA	agtctgcaagactcctgcaagaccaattatatctgcagatctcg

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PF 14-MAR-1996; US-618236.

PR 14-MAR-1996; US-618236.

PR 14-MAR-1996; US-618236.

PR (GETH) GENENTECH INC.

RGETH) GENENTECH INC.

RGETH) GENENTECH INC.

RGETH) GENENTECH INC.

ROSENTAR ROSENTHAL A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

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PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

PI Klein RD, Moore MW, Rosenthal A, Rosenthal A, Rosenthal A, and 
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Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;

GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.

Mus musculus.
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                                                                                                CCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGAGAACTACGCAGACTGCCTCCTGGCC
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Pred. No. (
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d. No. 0.00e+00;
Mismatches 46;
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PT Isolated glial cell derived neurotrophic factor receptor alpha - product grant collection and treat associated grant itself collection and treat associated products; particularly enteric nervous system or kidney disorders products; particularly enteric nervous system or kidney disorders products; particularly enteric nervous system or kidney disorders products and collection and collection alpha (GDNFR alpha) (CT play 1327) clone 26; the 3' end of the clone is given in created collection and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1998 (first entry)
Mouse GDNFR alpha clone 26 5' end.
Glial cell derived neurotrophic fact
GDNF; mouse; kidney disease; glomeru
Mus musculus.
Key
Location/Qualifiers
CDS
287. 418
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13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
(GETH ) GENENTECH INC.
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Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                       Klein RD, Moore MW, Rosenthal A, Ryan WPI; 97-470819/43.
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Isolated gilal cell derived neurotrophic factor receptor alpha - Isolated gilal cell derived neurotrophic factor receptor alpha - Isolated gilal cell derived neurotrophic factor receptor alpha - Isolaters, particularly enteric nervous system or kidney disorders is Example 1; Page 6; 100pp; English.

Chis DNA sequence comprises a human EST-derived sequence designated (Critical County) in the catter receptor (CDNFR) sequences, including human country particularly also suitable as probes for GDNFR sequences are another human EST-derived sequence designated ye83h05.r1 (see T84978), and critical country and these EST-derived sequences (see T84980-81) or proteins encoded by them. The invention relates to notive rat (GDNFR and its receptor. In particular, it relates to native rat (GDNFR alpha to see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha,
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Best Local :
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W09733912-A2.

18-SEP-1997; U04363.

13-MAR-1996; US-618236.

14-MAR-1996; US-618236.

14-MAR-1996; US-618202.

(GETH ) GENENTECH INC.

Klein RD, Moore MW, Rosenthal A, Ryan AM
WPI; 97-470819/43.
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365; Conser
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Klein RD, Moore MW, Rosenthal A, Ryan AM:

WFF; 97-470819/43.

WFF; 97-470819/43.

Yf Isolated gilal cell derived neurotrophic factor receptor alpha -

Yf useful to develop products to diagnose and treat associated

disorders, particularly enteric nervous system or kidney disorders

Example 1: Page 61: 100pp; English.

Example 1: Page 61: 100pp; English.

This DNA sequence comprises a human EST-derived sequence designated

Ye83h05.rl. It can be used to identify gilal cell derived

neurotrophic factor receptor (GDNFR) sequences, including human

Ye83h05.rl. It can be used to identify gilal cell derived

ye83h05.rl. It can be used to DNFR sequences are another

human EST-derived sequence designated y170a10.rl (see T84979), and

fragments. Also suitable as probes for GDNFR sequences are another

human EST-derived sequence designated y170a10.rl (see T84979), and

fragments of these EST-derived sequences (see T84980-81) or

proteins encoded by them. The invention relates to native rat

GDNFR and its receptor. In particular, it relates to native rat

GDNFR alpha (see W77327), its variants and soluble derivatives

(extracellular domain), chimeric GDNFR alpha and antibodies which

bind to the GDNFR alpha, including agonist and neutralising

antiodies, as well as various uses for these molecules. It also

relates to assay systems for detecting ligands to GDNFR alpha,

systems for identifying GDNF-related conditions, methods for
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Best Local S
Matches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1997.
13-MAR-1997; U04363.
14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human EST-derived sequence ye83h05.rl.

Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
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WO9733912-A2
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71.7%;
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Pred. No. 1.41e-7
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                                                                                                                                                                                                                                                    Query Match 5.2%;
Best Local Similarity 100.0%;
Matches 112; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                        proliferation capacity—and its components and derived antibodies, useful in diagnosing malignant tumours.

Claim 1, Page 73; 106pp; German.

The DNA shown is found in human or animal cells that have an unlimited capacity for unlimited cell proliferation or tumour formation. They have no ability to promote immortalisation of the cells, and are usually found in a DNA-protein complex in the cell cytoplasm. The DNA is useful for detection of these complexes, and diagnosis of malignant tumours. Differentiation between cells with unlimited and only transient proliferation is possible. (See also Q85493-54)

Sequence 385 BP; 121 A; 83 C; 90 G; 91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identifying molecules homologous to GDNFR alpha, and claimed methods for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system related disorders. Transgenic and knockout animals are also claimed.

Sequence 351 BP; 77 A; 117 C; 96 G; 57 T;
                                                                                                                             1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 95-067344/09.

New DNN-protein complex characteristic of cells with unlimited new DNN-protein capacity - and its components and derived antibodies.
   1131 GTCTTAAGGAGAACTACGCAGACTGCCTCCTGGCCTACTCGGGACTGATTGG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-1995.
13-JUL-1994; E02307.
15-JUL-1993; DE-233727.
(BOEF ) BOEHRINGER MANNHEIM GMBH.
Abken H, Albert W, Jungfer H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnose; malignancy; biopsy; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-1996 (first entry)
DNA probe 32 detects DNA-protein complex in immortal cells
DNA-protein complex; detection; proliferation; tumour form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q85526 standard;
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Similarity 73.1%;
212; Conservative
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Pred. No. 1.25e-57;
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Pred. No. 1.01e-64
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                                                                                                                                                                                                                                                                                                                   Length 385;
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   PRO XXX DO A C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT Isolated glial cell derived neurotrophic factor receptor alpha - pri useful to develop products to diagnose and treat associated pri useful to develop products to diagnose and treat associated pri useful to develop products to diagnose and treat associated pri useful to develop products to diagnose and treat associated pri useful to disorders prize a proper to designated yi70al0.rl (see T8479). It can be used as captured developed to dentify glial cell derived neurotrophic factor receptor (GDNFR) sequences, including human variants. The invention relates to novel uses of GDNF and its receptor. In particular, it relates to rat GDNFR alpha (see W27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which compared to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also crelates to assay systems for detecting ligands to GDNFR alpha, compared to the compared to the physiological role of GDNF, diagnostic conditions, methods for the treatment of GDNF-related conditions, methods for checknidges for identifying GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with related and knocknut animals are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Human EST-derived sequence y170a10.rl fragment.
Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
                               expressed sequence Homo sapiens. W09733912-A2.
                                                                              27-APR-1998 (first entry)
Human EST-derived sequence ye83h05.r1 fragment.
Glial cell derived neurotrophic factor receptor alpha;
GDNF; human; kidney disease; glomerulonephritis; therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC. Klein RD, Moore MW, RC WPI; 97-470819/43.
                                                                                                                                                   T84980;
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14-MAR-1996; US-618236.
14-MAR-1996; US-615902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; ss.
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18-SEP-1997.
13-MAR-1997; U04363
                                                                                                                                                                          T84980
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                                                                                                                                                                                                                                                                                                                               aagtgccacaaggccctgcgccagttcttcgaccgggtgcccagcgagtacacctaccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAACTGCCTGGACGCAGCCAAGGCCTGCAACCTGGACGACACCTGTAAGAAGTACAGG
                                                                                                                                                                                                                                          ATGCTCTTCTGCTCCTGCC
                                                                                                                                                                                                                                                                                                           AAGTGCCACAAGGCCCTCAGGCAGTTCTTCGACAAGGTTCCGGCCAAGCACAGCTACGGG
                                                                                                                                                                                                                                                                                                                                                                             TCGGCCTACATCACCCCCTGCA-CCACCAGCA-T-GTCCAACGAGGTCTGCAACCGCCGT
                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155;
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Similarity 77.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore MW, Rosenthal A, Ryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and knockout animals are also claimed. 201 BP; 41 A; 78 C; 46 G;
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                                                                                                                                                                      DNA;
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Pred. No.
0; Misma
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2.10e-46;
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                                                                                   therapy;
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                                                                                                      GDNFR alpha;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to rat GDNFR alpha (see w27327), its variants and soluble derivatives (extracellular domain), chimeric GDNFR alpha and antibodies which bind to the GDNFR alpha, including agonist and neutralising antiodies, as well as various uses for these molecules. It also relates to assay systems for detecting ligands to GDNFR alpha, systems for studying the physiological role of GDNF, diagnostic techniques for identifying GDNF-related conditions, methods for identifying molecules homologous to GDNFR alpha, and claimed methods for the treatment of GDNF-related and GDNFR alpha-related conditions, particularly kidney disease associated with glomerulonephritis and enteric nervous system related disorders. Transgenic and knockout animals are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated glial cell derived neurotrophic factor receptor alpha useful to develop products to diagnose and treat associated disorders, particularly enteric nervous system or kidney disorders Example 1; Page 61; 100pp; English.

This DNA sequence comprises a fragment of a human EST-derived sequence designated ye83h05.rl (see T8497B). It can be used as a probe to identify glial cell derived neurotrophic factor receptor (GDNFR) sequences, including human variants. The invention relates to novel uses of GDNF and its receptor. In particular, it relates
Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                               01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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Klein RD, Moore MW
WPI; 97-470819/43
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EP-571911-A.
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14-MAR-1996;
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155; Conser
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US-615902.
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Pred. No.
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2.10e-46;
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051746
051746;
Disclosure; p; English.

Random point mutations were introduced into the alpha fragment E.Coli beta-galactosidase. The wild type sequence was obtained single stranded template and an oligonucleotide was hybridised
                                                                                                                                                                                                                                                                                                                                                                                                                              Base substituted E.coli beta-galactosidase alpha-fragment. E.coli beta galactosidase alpha-fragment; base substitutions; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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                                                                           Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                 EP-285123-A.
05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
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24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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                                                                                                                                                (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J,
WPI; 88-279927/40.
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08-NOV-1990
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Similarity 8.9%;
5; Conservative
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probe MK14-A
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187..204
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E.coli beta-galactosidase alpha-fragment.
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                                                                                                              Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                 introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E. coll beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
transcriptase and the molecules are misincorporated by the
amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N81164;
N81164;
O8-NOV-1990 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                      occurred singularly in any
See also P80575.
Sequence 204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Base substituted E.coli be E.coli beta galactosidase Escherichia coli.
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Sequence 204 BP; 21 A; 47 C; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-1987; US-034819
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     GCCGGTTAACAGCAGGTTGTCAGATATATTCCGGGCAGTCCCGTTCATATCAGATGTTTT 726
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                            CTGAAGTTGGTTTCCTTGCCCGCCACGCACTGCCTTAGTGTGCGGTACTTGGTGCTGCAG 424
                                                                                                              Similarity
12; Conse
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36; Conser
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.uted E.coli beta-galactosidase alpha-fragment.
galactosidase alpha-fragment; base substitutions;
                                                                                                              1.9%;
larity 11.7%;
Conservative
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/function-multiple cloning
187..204
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                                                                                                              Score
Pred.
55; M
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Pred. No. 3.11e-11;
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                                                                                                                                                                                                                            47 C;
                                                                                                              Mismatches
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                                                                                                                                        40; DB 1; I
No. 1.99e-09;
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RESULTATION OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                              PT Identifying proteins or peptide(s) which bind a ligand - by Identifying a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a peneric DNA sequence used to generate random TSAR (Totally CO 70468 is a generic DNA sequence used to generate formula can also be crepresented as follows: X(NNB)11(TGC)(NNB)52(NNB)7(TGC)(NNB)10Y X CO and Y are flanking restriction sites (X is not the same as Y) that are contained for the specific peptides generate by these generic sequences are shown in Q70466-68. CC Other specific peptides generated by these generic sequences are shown in CR5151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with CC cafinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with CC cafinity for a ligand and a second effector peptide portion that is comprising the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. These residues confer some degree of conformational rigidity to the peptides. The TSARS CC or compsons, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, call of the conformation of macromolecules, eg. motal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                   Query Match
Best Local s
Matches
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31-JAN-1994; US-18933
(UYNC-) UNIV NORTH CA
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
P-PSDB; R65154.
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18-AUG-1994.
01-FEB-1994;
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Q70468;
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   CAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGAC
                                                                                                                           CATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTTCGA 903
                                                                                                                                                              bnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnnnnnnn
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                1.8%;
larity 4.5%;
Conservative
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NORTH CAR
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US-1765.00.
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34; Misma
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6, 9 or 12 nucleotides (se
                                                                                                                                                                                                                                                      Mismatches
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. 3.05e-08;
. Thes 73;
                                                                                                                                                                                                                                                                                                             Length 114;
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18-AUG-1994; U00977.
01-FEB-1994; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLJ
FOWIKES DM, KAY BK;
WPI; 94-279739/34.
                 070469 Standard; DNA; 114 BP.
070469;
07-APR-1995 (first entry)
08-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding dom
effector domain; concateneated heterofunctional protein; linker;
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Q70465;
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                        CATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTTCGA 903
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/note= "this sequence represents 'Z'; Z
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Pred. No. 3.05e-08;
34; Mismatches 73;
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CC O70469 is a generic DNA sequence used to generate random TSAR peptide (TGC)(NNB)52(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction cc sites (X is not the same as Y) that are not specified further. This considered by these generic sequences are shown in 070465-68. Other specific peptides concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated by these specific peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonuclectides are also designed in, or flanking, the contains 2 or 4 cysteine residues positioned in, or flanking, the contains 2 or 4 cysteine residues. These residues confer some degree of contains 2 or 4 cysteine residues. These residues confer some degree of contains 2 or 4 cysteine residues. These residues confer some degree of contains 2 or 4 cysteine residues. These residues confer some degree of contains 2 or 5 cysteine residues. These residues confer some degree of contains 2 or 5 cysteine residues. These residues confer some degree of contains 2 or 5 cysteine residues. These residues confer some degree of contains 2 or 5 cysteine residues. The stars or compans. comprising conference active modelies, eg. monoclonal or polyclonal antibodies conference and conference active models of hybridoma conference active models of hybridoma conference active models and activity a
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Release 3.1A John F. Collins, Biocomputing Research U Copyright (c) 1993-1998 University of Edinburgh, U.K Distribution rights by Oxford Molecular Ltd	
MPsrch_nn n.a n.a. database search, using Smith-Waterman algorithm on: Wed Jun 24 22:01:59 1998; MasPar time 2326.45 Seconds 1227.537 Million cell updates/secrabular output not generated.	
Title: >US-08-866-354-3 Description: (1-2138) from US08866354.seq Perfect Score: 2138 N.A. Sequence: 1 AGCTCGCCTCCCCGGGGCAGAGACAGGCCCGCAGCCGTCG 2138 Comp: TCGAGCGAGAGGGCCCCCTCTCTGTCCGGGCGTCGGCAGC	
Scoring table: TABLE default Gap 6	
Nmatch STD: Dbase 0; Query 0	
Searched: 1759237 seqs, 667866413 bases x 2 Post-processing: Minimum Match 0%	
miscing first 4	
Database: genbank-est1 2:em_est3 Database: genbank-est106 1:em_est1 2:em_est3 genbank-est106 3:gb_est14 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 12:gb_est18 13:gb_est15 14:gb_est2 15:gb_est20 16:gb_est21 17:gb_est21 18:gb_est3 19:gb_est4 20:gb_est5 21:gb_est6 22:gb_est7 23:gb_est8 24:gb_est9 25:gb_gss 26:gb_sts	
catistics: Mean 11.800; Variance 1.984; scale 5.947	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES ID Description Pred. N	
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149 7.0 330 9 AA573164 nm51f06.s1 NCI_CGAP_Br 141 6.6 266 7 AA471183 PMY2139 KG1a Lambda Za 119 5.6 521 18 H12881 y170a10.r1 Homo sapien	
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ALIGNMENTS

FEATURES source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	NID NET KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION ACCESSION
Seq primer: -28m13 rev2 ET from Amersham Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 259. Location/Qualifiers 1. 631 /organism="Mus musculus" /strain="C3H"	Washington University School of MedicineP Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:524073	Theising, B. Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The WashU-HHMI Mouse EST Project Unpublished (1996)	Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 631) 1 (bases 1 to 631) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Marra,M., Mucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Ceisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,	g2259047 eST. house mouse. house musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	AA518362 631 bp mRNA EST 16-JUL-1997 v110d02.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone 903363 5', mRNA sequence. AA518362

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KEYWORDS
SOURCE
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/cell_line="C2C12"
/lab_host="DH10B"
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                  181 ATCTCGCCTTGCAGATITTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTG 240
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                                                                                                                                                                61 GGACGTCGCCTGCACCGAGAGGCGGCGACAGACTATCGTCCCTGTGTGCTCCTATGAAGA 120
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                 l Similarity
427; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
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/clone="774901"
/clone_lib="Ko mouse e
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                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:232784
Seq_primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 465)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Unpublished (1996)
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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314 286 1810
                                                                                        quality sequence stop: 347.
                                                                                    M.Fatima Bonaldo."
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc
/lab_host="DH10B"
                                                            /db_xref="taxon:10090"
/clone="371352"
                                                 /clone_lib="Soares mouse
                                      /sex="unknown"
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1 (bases 1 to 430)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., and
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:245779
                                                                                                                      Contact: Marra M/Mouse EST Project
Washdr-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. La
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/note="vector"
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/dev_stage="13.5-14.5dpc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:420598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
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                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                  /clone_lib="Soares m
/tissue_type="Liver"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="680894"
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                         .>478
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1 GCTAATTTGCAGGCACAGAAGCTGAAATCCAATGTATCGGGCAGTACACATCTCTGTCTT
                   CCAGTTTTAAAAGCTCGGTTGAGAAGCAGTTTCACCCAGCGGGAACTCCTTTGTTGTTTT 352
                                                                                                                                                                                                                                            CTGGCTGCCCTGTTGTCTGTATCATTGGCAGAAACATCGTAGCTGCATCC-----AG
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                                                                                                        TATGAAAAGACAAAAGAGAACCAAGTATTCTGTCCC-TGTCCTCTTGTATATCTGAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washn-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 313; DB 24; Pred. No. 0.00e+00;
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                         TAAAGATAATAGGGTGGACAGAGCGGTTACCACCAGGACCAGCAGTGGGCTCAGACCACA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAACTCAGAAAACTCTGGGGCATGGTGTGGCTTCAGGGGACTGTTTTGTAACCTG
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    TACAGATAACAGGGCAGCAAGGGCGGTGAGCATCAGCACCGGCAGTGAGCTCAGACTGCA 1628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nh91b04.sl NCI_CGAP_Brl.1 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AA512935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 1735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                      Similarity
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                                                                                 14.2%;
larity 85.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert_Strausberg@nih.gov
                                                                                                                                                                                                                        /clone="IMAGE:965839"
/clone_ib="NCI_CGAP_Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                            /Organism="Homo sapiens"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker: lst strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is not normalized. (The normalized version of this library is NCI_CGAP_Br2.) Library was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                               Score 303; DB 7;
Pred. No. 0.00e+00;
0; Mismatches 65
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IMAGE:965839,
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1 (bases 1 to 439)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vu96d10.rl Stratagene mouse skin
1210003 5', mRNA sequence.
AA727460
                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
                                                                                                                                                                                                                                      primer: -28ml3 rev1 ET from h quality sequence stop: 436.
                                  /note="Organ: skin; Vector: pBluescript SK-; Site_1: ECORI, Site_2: XhOI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
sequence: 5' CTCGAGTTT
/db_xref="taxon:10090"
/clone="1210003"
                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6"
                                                                                                                                                                                                               Location/Qualifiers
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
MGI:418844
Seg primer: -28m13 ro...
                                                                                                                                                                                   1 (bases 1 to 459)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. LC
                                                                                                                                                                                                                                                                                                                                                                                   AA245689
mx03e07.rl
                                                                                                                                                              Unpublished
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Vertebrata; Eutheria; Rodentia; Sciurognathi; I
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Unpublished (1996)
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Pred. No. 0.00e+00;
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Best Local Similarity 80.1%;
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                           AA573164
nm51f06.s1
                                                                                                                                                                                                                                                                   sequence.
AA573164
g2347692
Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                           Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                              1 (bases 1 to 330)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                   Unpublished (1997)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="679140"
/clone=1b="Soares mouse N
/tlssue_type="tLver"
/lab_host="DH10B"
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Pred. No. 6.37e-300;
0; Mismatches 54;
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found through the I.M.A.G.E. Consortium/LLNL at:

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RESULT 10
LOCUS
DEFINITION
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AUTHORS
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Best Local Similarity 83.1%;
Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAAGATAATAGGGTGGACAGAGCGGTTACCACCAGGACCAGCAGTGGGCTCAGACCACA 137
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                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
AA471183
g2199040
Contact: Hawley RG
Oncology Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
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                                                                                                                                  1 (bases 1 to 266)
Claudio, J.O., Liew, C.C. and Hawley, R.
Hematopoletic progenitor ESTs
Unpublished (1997)
                                                                                                                                                                                                                                                       Eukaryotae;
Vertebrata;
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                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                      numan.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I collog(dT) primer: Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector: This library is the normalized version of NCI_GAP_Br1.1 Library was constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="IMAGE:1071779"
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/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                       mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; HC
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da Zap Express cDNA Library Homo
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Pred. No. 1.20e-273;
0; Mismatches 39;
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EST.
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Fax: 416 3403453

Email: r.hawley@utoronto.ca

Email: r.nawley@utoronto.ca

Charley arandomly picked from subtracted KGla primary cDNA
           Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osi
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Ho
                                                                                                                  y170a10.rl Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 6.6%;
1 Similarity 84.2%;
223; Conservative
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/note="Vector: Lambda Zap Express (Stratagene); Site_1:
ECORI; Site_2: XhoI; Unidirectional cloning sites:
ECORI-XhoI mRNA was purified from KGla cell line, cDNA
was synthesized using an XhoI-OlloyedT linker primer.
ECORI adaptors were ligated, followed by digestion with
XhoI for directional cloning into predigested Lambda Zap
Express."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="KG1a Lambda Zap
/cell_type="promyeloblast"
/cell_line="KG1a"
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 Clark, N.,
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74 c
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Pred. No. 1.21e-254;
0; Mismatches 34:
Dubuque, T., Elliston, K.,
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cDNA clone 43207
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                                                                                      5.6%;
l Similarity 75.3%;
213; Conservative
Eutheria, Primates; Catarrhini, Ho
(bases 1 to 229)
Hiller, L., Clark, N., Dubuque, T.,
Holman, M., Hultman, M., Kucaba, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stops: 278 source: IMAGE Consortium, LINL; This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest park Parkway, Box 8501, St. J Tel: 314 286 1810

Fax: 314 286 1810
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                                                                                                                                                                                                                                                                             ye83h05.rl
R02249
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WashU-Merck EST Project
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                                             Eucaryotae; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
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/clone="43207"
154 c 144 g 11
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Pred. No. 6.57e-203;
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               Elliston, K., Hawkins,
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 Lennon, G., Marra, M.,
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nl Similarity 75.3%;
171; Conservation
                                                                                                                                                                                                                                                                                                                                                             92801165
EST.
                                                                                                                                                                                                                                                                                        Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; I
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                                                 Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                             97SN1787 Rice Immature Seed Lambda cDNA clone 97SN1787, mRNA sequence AA754459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
High quality sequence stops: 214
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
                                                                                                                                      Contact: Eun M.Y.
                                                                                                                                                                      Unpublished (1998)
                                                                                                                                                                                                      1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
WashU-Merck EST Project
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Unpublished (1995)
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/clone="124377"
, 85 c 55 g 3
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1. .229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 HYWBVBNTKVDVGNHTRCSRWRBVTR-MAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIRATRSYTCVRKYCVMWMIKKVVKKYHVVBBGCHBIDSKCK 237
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                                                                                                        Contact: Eun M.Y.

Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA

Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.

Seq primer: M2025270400011fiers
                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; L
Poales; Poaceae; Oryza.
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larity 12.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
/organism-"Oryza sativa"
/orlitivar-"Milyang23"
/orle-"Vector: pBluescript SK(+); Site_1: Ecc
/note-"Vector: Dbluescript SK(+); Site_1 to
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Pred. No. 3.14e-75;
115; Mismatches 78; Indels
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CDNA Library Oryza sativa
  ECORI; Sit
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                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 CWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRAT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSYTCVRKYCVMWMTKKVVKKYHVVBBGCHBTDSKCKTMWMTNKHVMTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                         seq primer: -28m13 rev2 ET from Amersham
H1gh quality sequence stop: 438.
                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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llarity 9.6%;
Conservative
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/clone_11b="Rice Immature Seed Lambda
/tissue_type="immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
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/db_xref="taxon:4530"
/clone="97SN1787"
                                                                                                                                                       ocation/Qualifiers
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; Pred. No. 4.79e-71;
119; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NML Mus musculus cDNA clone 748642 5', mRNA
                                                                                                                                                                                                                                                                                                                              Louis,
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Search completed: Wed Jun 24 23:10:00 1998 Job time : 4081 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: bular output not generated. Tue Jun 23 18:34:40 1998; MasPar time 15.71 Seconds 456.813 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-08-866-354-4 (1-468) from US08866354.pep 3384

Scoring table: PAM 150 Gap 11 1 MFLATLYFALPLLDLLMSAE......PVLMLTALAALLSVSLAETS 468

124785 seqs, 15338987 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 34.847; Variance 146.333; scale 0.238

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result No.
3384 955 959 971 971 971 971 971 971 971 971 971 97	Score
100 200 200 200 200 200 200 200 200 200	Query Match
468 355 316 316 376 676 769 947 947 95 285 285 285 285 285 285 285 285 285 28	Length
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W27327 P8825885 W15023 W150258 W35825 W424256 W6015252 W601770 W601771 P801760 P811769 P811769 P811769	Ħ
Rat glial cell derive vascular endothelial sequence encoded by L C-mpl ligand variant Mpl ligand analogue, Pseudorables virus (B Human CD18 for use in Beta-subunit CD18 of Amino acid sequence o Carbohydrate binding Rat carboxypeptidase Li-3 variant/Fxa/GlyS IL-3 variant/Fxa/GlyS IL-3 variant/c-mpl ligand Sequence of the gag p Fusarium oxysporum c-Sequence encoded by t pl7 antigen of human The sequence encoding	Description
0.000 0.000 1.89e+01 1.89e+01 3.66e+01 3.66e+01 3.66e+01 5.06e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01 8.20e+01	Pred. No.

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mbinant beta ence of clon	Sequence or rusion pr	transporter	V-III gag/	_	gene	V-80)(GAG-VII)(-gag protein.	HIV-gag internal prot	lence of LAV vi	uence		sequence encodin	of g	polyprot	'-1 gag pro	gag encoded by v	ligand analogue,	d by	HIV-1 MA delta-105-11	HIV-1 MA delta-5-16 m	140	HTLV-IIIb p17 sequenc
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Best Loc
Matches
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                                                                                                                                                                                                         Vascular endothelial growth factor 2.
VEGF2; vascular endothelial growth factor; vascular permeability factor;
PDGF family; anglogenesis; induce growth; bone.
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R82686 standard; Protein;
R82686;
R82686;
(first entry)
misc_difference
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                                                                                                           misc_difference
                                                                                                                                        protein
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Similarity 100.0%;
468; Conservative
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87
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/note=
96
                                                                                                           /label mature_protein 62
                           /note=
93
                                                                               /note-
85..98
                                                                                                                                         /label= signal_peptide
25..350
                                                                                                                                                                               Location/Qualifiers
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                                                                                              "conserved
           "conserved cys"
                                     "conserved cys"
                                                                  "signature
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                                                                    for the PDGF/VEGF family'
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pr used for prodn. of DNA, antigens and antibodies used in
rediagnosis of AIDS and pre-AIDS
rediagnosis of AIDS and pre-AIDS
rediagnosis of AIDS and pre-AIDS
rediagnosis of AIDS and LAV MA L (N80437) were isolated from the peripheral
LAV EL I (N80436) and LAV MA L (N80437) were isolated from the peripheral
blood lymphocytes of patients. Different AIDS virus isolates concerned
care designated by 3 letters of the patients name. Stable probes including
the DNA sequences can be used for detection of the new LAV viruses or
related viruses or DNA proviruses in ep. biological samples. The proteins
or peptides can be used for detection of antibodies induced in vivo and
present in biological fluids. The DNA can also be used for the expression
of LAV viral antigens for the prodn. of a vaccine against LAV. The
collapse tides can also be used for the prodn. of antibodies for the
Category for the proteins related to the LAV viruses, partic. for diagnosis
of AIDS or pre-AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human vascular endothelial growth factor 2 polypeptide - used to provide diagnostic, therapeutic and/or prophylactic effects against various diseases, esp. in wound healing and periodontal disease Sclaim 1; Fig 1A-D; 48pp; English.

This full length vascular endothelial growth factor 2 (VEGF2) comprises 350 amino acids of which approx. the first 24 amino acids represent the leader sequence. VEGF2 is structurally related to the VEGF/PDGF family. It is partic. important that all eight cysteines are conserved within the members of the family. In addition, the signature for the PDGF/VEGF family, pxCYXXXCXGCCN, is conserved in VEGF2. VEGF2 induces growth of damaged bone, peridothum or ligament tissue. It is used for the promotion of endothelialisation in vascular graft surgery. Since anglogenesis is important in keeping wounds clean and non-infected, VEGF2 may be used in association with surgery and following the repair of cuts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-1995.
12-MAY-1994; US-207550.
08-MAR-1994; US-207550.
(HUMA-) HUMAN GENOME SCI
Cao L, Hu J, Fraser Ch
WPI: 95-328266/42.
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22-JUN-1987; E00326.
23-JUN-1986; EP-40138.
(INSP) Inst Pasteur.
Alizon M, Sonigo P, W
WPI; 88-014396/02.
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misc_difference 104
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Sequence encoded by LAV MA L GAG gene
HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
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Similarity 23.2%;
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2.23e+01;
-~hes 26;
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                                                               RESULT
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Best Local Similarity 41.9%;
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Best Local
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 16-APR-1997
Mpl ligand an
Native human
                                                                                                                                                                                                                                                                                                     Novel c.mpl receptor agonist polypeptide(s) - stimulate haematopoietic cell production, useful in thrombocytopenia treatment and selective ex vivo expansion of haematopoietic stem cells Example 6; Page 61-62; 151pp; English.

This polypeptide is a c.mpl ligand variant comprising amino acid residues 1-153 of c.mpl ligand (see W1996) fused via a linker (W15003) to amino acids 1-153 of c.mpl ligand and be used as a PCR template for generating novel forms of c.mpl ligand. Specifically claimed circularly permuted variants of c.mpl ligand (see W15005-16) are useful in the treatment of thrombocytopaenia and selective ex vivo expansion of haematopoietic stem cells.
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Chimeric H
Chimeric S
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C-mpl ligand; thrombopoietin;
haematopoietic cell; stem cel
                                      W12929 standard;
W12929;
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05-OCT-1995;
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01-JAN-1998
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                                                                                                                         ligtglp
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                                                                                                                                                                                                      IQAFGNGSDVTMWQPAPPV-QTTTATTT-TAFRVKNKPLGPAGSENEIPTHVLPPCANLQ 399
                                                                                                     LLSVSLA
                                                                                                                                                      AQKLKSNVSGS-THLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAA
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                                                                                                                                                                                                                                                      h 2.7%;
Similarity 22.0%;
28; Conservative
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7 (first entry)
analogue, [Asn54, Ser56] mpl ligand.
an mpl ligand; altered glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summers NL;
                                                                                                                             276
                                                                                                     465
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164..3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                  Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McKearn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "c-mpl(1-153)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tin; receptor; agonist; cytokine; human;
cell; thrombocytopaenia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316
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Pred.
                                                                                                                                                                                                                                                       Score 91; DB 24;
Pred. No. 4.31e+01
34; Mismatches 6
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No. 1.89e+01
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Best Local S
Matches 2
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30-DEC-1983; 567018.
30-DEC-1983; US-567018.
30-DEC-1983; US-567018.
(BAYU) Baylor College of (NOVA-) Novagene Ltd.
Kit M, Kit S;
Temp. resistant pseudorables virus - useful in vaccines as virus does not produce thymidine kinase. Disclosure; Fig. 5; 26pp; English.

The pseudorables virus (BUK-7)CC thymidine kinase coding sequence be mutated using a mutagen or deleted, so producing a virus (which is also modified to be temperature sensitive) which cannot produce functional thymidine kinase. Such a mutant is useful in a vaccine to control the spread of pseudorables virus. Vaccinated animals are also less likely to become carriers of the virus, and unlikely to require a dormant infection with pathogenic field strains. The mutagen-induced mutant is pseudorables virus (BUK 5A0 ATCC VR-2078, and may be lyophilised for storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page : 106pp; English.

The sequences given in W1291-54 represents claimed analogues of native human mpl ligand. These analogues have altered glycosylation patterns. Alteration of glycosylation of mpl ligand can cause improved biological activity. The mutated proteins comprise a greater or lesser number of carbohydrate defines and higher or lower shallc acid content than wild type mpl ligand. Compositions comprising these mpl ligand analogues may be used to treat diseases involving an existing or expected megakaryocyte/platelet deficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elliott SG;
WPI; 96-393399/39.

MPI ligand analogue has sequence with added, deleted glycosylation site(s) - useful in compsns. to treat thrombocytopaenia
Claim 8; Page -; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-1995; US-38
09-FEB-1996; US-59
(AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbohydrate side chain; sialic acid megakaryocyte/platelet deficiency.
                                                                                                                                                                              N-PSDB; N50286.
                                                                                                                                                                                                                                                                                                     US4514497-A.
                                                                                                                                                                                                                                                                                                                  Pseudorabies virus
                                                                                                                                                                                                                                                                                                                                               Pseudorables virus (BUK-7); thymidine kinase; mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                            P50258;
22-NOV-1991
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                                                                                                                                                                                              WPI; 85-122203/20.
                                                                                                                                                                                                                                                                                                                                 temp. resistance; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
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22; Conse
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US-388779.
US-591070.
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larity 23.2%;
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Pred.
29; M
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d. No. 5.06e+01;
Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                  PT lymphocyte veto molecule comprising response cell activating protein linked to molecule that targets stimulator cell marker, protein linked to molecule that targets stimulator cell marker, provided for selective suppression of immune response, e.g. prevention profession of the protein of graft rejection or treatment of auto-immune disease call in selection or treatment of auto-immune disease protein selective veto molecule is a chimeric molecule can protein polypeptide that binds a molecule, which differentiates can be used to a tragetting polypeptide that binds a molecule, which differentiates can be regulated in the autoimmune response.

CC a host cell from a tissue graft cell, or selectively targets a stimulator cell involved in the autoimmune response and constitution to call the protein binds a molecule that targets can be used to suppress an immune response and constitution of autoimmune diseases, e.g. systemic lupus carthematosus, myasthenia gravis, rheumatoid arthritis, insuling carthematosus, myasthenia gravis, rheumatoid arthritis, insuling can be molecule that differentiates graft and constitution of the protein binds a molecule that differentiates graft and constitution. The veto molecule can be used to reduce transplant rejection. The veto molecule can be used to reduce transplant to autoantigus, but leave other stimulator cells unaffected, e.g. containing egeneralised immuneraceion.
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10-APR-1997; U05943.
10-APR-1996; US-630172.
(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
STBERZ UD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1998 (first entry)
Human CD18 for use in T lymphocyte veto molecule.
Human; CD18; T lymphocyte veto molecule; chimeric molecule;
targetting polypeptide; suppression; immune response; treatment;
autoimmune disease; allergy; immunological disorder;
transplant rejection.
15-JUL-1992 (first entry)
Beta-subunit CD18 of leukocyte integrin.
                R24256;
15-JUL-1992
                                        T 8
R24256 standard; Protein; 769
                                                                                                                                                                                                                                                                                                            minimise generalised immunosuppression. Sequence 676 AA;
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                                                                                                                                                                              QVEHISKGNNCLDAAKAC-NLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDK 202
                                                                                                                                                                                                           dtqyigkncecqtqgrssqelegscrkdnns-ii-cs-glgdcvcgqclchts----
                                                                                                                VPAKHSYGMLFCSCRDIACTER
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Similarity 29.3%;
24; Conservative
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Similarity 23.9%;
11; Conservative
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                                                                                                                                              521
                                                                                                                                                                                                                                           Score 90; DB 27;
pred. No. 5.06e+01
22; Mismatches 2
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Pred. No.
15; Misma
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3.66e+01
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Matches 2
             Homo sapiens.
W09737016-A1.
09-OCT-1997.
01-APR-1997; IL0117.
26-AUG-1996; IL-119133.
02-APR-1996; IL-117800.
(YEDA) YEDA RES & DEV C
Boldin M, Kovalenko A, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide(s) derived from beta sub-unit CD18 of leukocyte integrins - prevent leukocyte binding to ICAM and leukocyte chemotaxis, for treating inflammatory diseases and rhinoviral infection Disclosure; Fig 1; 31pp; English.
This sequence is the beta-subunit, CD18, of the leukocyte integrins. Peptides were designed based on the beta-subunit sequence and were tested for activity in the leukocyte/endothelial cell adhesion assay. See R22104-R22112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09203473-A.
05-MAR-1992.
23-AUG-1991;
27-AUG-1990;
                                                                                                                                                            15-APR-1998 (first entry)
Amino acid sequence of NF-kappaB inducing kinase.
Human tumour necrosis factor receptor-associated factor 2; TRAF2;
TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction;
intracellular signalling activity; acute hepatitis;
                                                                                                                                                                                                                                             W42402
W42402;
                                                                                                                                              autoimmune-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q22780
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Liu DY, Kaymakcalan Z, Mundy
WPI; 92-096833/12.
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                                                                                                                                                                                                                                                                                                                            HSYGMLFCSCRDIACTER
                                                                                                                                                                                                                                                                                                                                                                                            ISKGNNCLDAAKAC-NLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAK 206
                                                                                                                                                                                                                                                            standard; Protein; 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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US-573624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intercellular adhesion molecule; endothelium;
ICAM-1; leukocyte chemotaxis; rhinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Peptide 3 (see R22106) tested for activity
leukocyte/endothelial cell adhesion assay"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Peptide 1 (see R22104) tested for activity in
leukocyte/endothelial cell adhesion assay"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukocyte/endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Peptide 6 (see R22109) tested for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%;
                                                                                                                                                cell
                Malinin
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Pred.
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5.06e+01
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RESULT
ID R11
AC R11
DT 122
DE CE
KW T1
PP 14
PF 08
PR 09
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CC The NIK or TRAF-2 binding proteins can be used for modulation or CC mediation in cells of NF-kappaB activity or any other intracellular CC signalling activity modulated or mediated by TRAF2. TRAF-binding proteins CC are especially used for prevention or treatment of pathological CC conditions associated with NF-kappaB induction, e.g. acute hepatitis, CC autoimmune-induced cell death, e.g. death of the beta Langerhans cells or the pancreas that results in diabetes, the death of cells in graft CC rejection, the death of oligodendrocytes in the brain in multiple CC sclerosis, and AIDS-inhibited T cell suicide which causes proliferation of the AIDS virus and hence the AIDS disease. The proteins are also useful for screening of ligands capable of binding to a protein, which are useful for modulating cellular activity modulated/mediated by TRAF2. Sequence 947 AA;
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                                                                                                                                                                                                                                                                    New fungal (hemi) cellulose degrading enzymes - for prodn. of liq. fuel gas and feed protein, have specified carbohydrate binding domain claim 20; Page 45; 73pp; English.

This CBD is homologous to a terminal A region of Trichoderma reesel cellulases and effects binding of a protein to an insoluble cellulosic or hemicellulosic substrate. It is one of ten specific CBD's (see R15244-R15253) which correspond to the generic CBD formulae in R15242 and R15243. The CBD is incorporated into a fusion protein comprising a catalytic domain from a cellulase, e.g. a second of the second constant of the constant 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1991.
08-MAY-1991. DK0124.
09-MAY-1990; DK-001158.
09-MAY-1990; DK-001158.
(NOVO ) NOVO NORDISK A/S.
(NOVO ) NOVO NORDISK A/S.
WOldike HF, Hagen F, Hjort CM, Hastrup WPI; 91-353766/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellulose; CBD; hemicellulosic substrate; Trichoderma reese1; cellulase; terminal A region. W0911/244-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1992 (first entry)
Carbohydrate binding domain #9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 32 AA.
                                                                                                                                         Similarity
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21; Conse
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larity 35.0%;
Conservative
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larity 28.8%;
Conservative
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  268
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Pred. No. 4
10; Mismai
                                                                                                                                         Score 87; I
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. 4.31e+01;
---hes 37;
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                                                                                                                                                                    DB 3;
                                                                                                                                            20e+01;
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Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified active recombinant carboxypeptidase B prodn. - by expressing DNA encoding the pro-enzyme, folding and enzymatic cleavage to give active form, used e.g. for insulin prodn.

Example 1; Page 36; 49pp; English.

The amino acid sequence of the activation peptide (W00601) of rat pro-carboxypeptidase B (pro-CPB) was deduced from a cDNA sequence (see also T35759) obtd. by PCR amplification of Sprague-Dawley rat pancreas cDNA. The sequence of the mature enzyme (W00602) has also been deduced. Pro-CPB can be expressed in host cells, e.g. Escherichia coli, and subsequently recovered, refolded and cleaved with trypsin to yield the active enzyme. CPB produced this way is cheaper than porcine pancreatic enzyme, and is free of other
                          This protein comprises interleukin-3 variant 13288 fused to FXa, a synthetic linker and amino acids 1-153 of c-mpl ligand. It is encoded by E. coli expression plasmid, pMON26640. The native c-mpl ligand is also referred to as Megakaryocyte Growth and Development Factor (MGDF) or thromobopoietin (TPO). Variants and chimera of c-mpl ligand can have an improved biological profile, such as increased activity and/or decreased side effects, and/or improved physical properties, such as improved half-life, stability and/or re-fold efficiencies. They can be used for selective ex vivo expansion of stem cells, for the treatment of patients having a haematopoietic disorder or in human gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1997 (first entry)
IL-3 variant/FXA/GlySer/1-153 c-mpl ligand fusion protein.
IL-3 variant/ Megakarycoyte Growth and Development Factor; MGDF;
c-mpl ligand; Megakarycoyte Growth and Development Factor; MGDF;
thromobopoletin; TPO; variant; mutein; chimera; increased activity;
decreased side effect; ex vivo expansion; stem cell; treatment;
haematopoietic disorder; gene therapy; human; interleukin-3.
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WPI; 96-362688/36.
N-PSDB; T35759.
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25-JAN-1996; U00995.
25-JAN-1995; US-378233.
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03-FEB-1995; US-383035
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                                                                                                                                                                                                                                                                                                              Example 12; Page -;
                                                                                                                                                                                                                                                                                                                                                                   Mutant c-mpl ligands haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 96-371436/37.
N-PSDB; T59355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staten NR;
WPI; 96-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
W09623888-A1.
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                                                                                                                                                                                                                                                                                                                                              disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.6%;
                                                                                                                                                                                                                                                                                                           74pp;
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pro-enzyme; protease;
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                                                                                                                                                                                                                                                                                                                 English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88; DB 18;
pred. No. 6.99e+01;
                                                                                                                                                                                                                                                                                                                                                                     for
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Best Local Similarity
Matches 27; Conser
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        This protein comprises interleukin-3 variant 13288 fused to a synthetic linker and amino acids 1-153 of c-mpl ligand. It is encoded by E. coli expression plasmid, pMON26471. The native c-mpl ligand is also referred to as Megakaryocyte Growth and Development Factor (MSDF) or thromobopoletin (TPO). Variants and chimera of c-mpl ligand can have an improved biological profile, such as increased activity and/or decreased side effects, and/or improved physical properties, such as improved half-life, stability and/or re-fold efficiencies. They can be used for selective ex vivo expansion of stem cells, for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-3 variant/GlySer/1-153 c-mpl ligand fusion protein.

c-mpl ligand; Megakaryocyte Growth and Development Factor; MGDF;
thromobopoletin; TPO; variant; mutein; chimera; increased activity;
decreased side effect; ex vivo expansion; stem cell; treatment;
haematopoletic disorder; gene therapy; human; interleukin-3.
W01760 standard; protein; 332
W01760;
29-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant c-mpl ligands - used haematopoietic cells and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 96-371436/37.
N-PSDB; T59356.
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03-FEB-1995; US-383035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
W09623888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W01771 standard; Protein; W01771;
                                                                                                                                                                                                                                                                                                                                              patients having a haematopoletic disorder or in human gene therapy.
Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 13; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baum CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1997 (first entry)
IL-3 variant/GlySer/1-153
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                                                                                             SLA
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                                                                                                                                                                       ktqmeetkaqdilgavtlllegvmaargqlgptclssllg-qlsgqvrlllgalqsllgt 242
                                                                                                                                                                                                                                          gsgggsnmaspappacdlrvlskllrdshvlhsrlsgcpevhplptpvllpavdfslgew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qlp 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gsgggsnmaspappacdlrvlskllrdshvlhsrlsqcpevhplptpvllpavdfslgew 183
                                                                                                                                                         KSNVSGS-THLCLSDSDFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSV
                                                                                                                                                                                                                     GNGSDVTMWQPAPPV-QTTTATTT-TAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKL 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ktqmeetkaqdilgavtlllegvmaargqlgptclssllg-qlsgqvrlllgalqsllgt 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNGSDVTMWQPAPPV-QTTTATTT-TAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLA 465
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Favara JP,
                                                                                                                                                                                                                                                                               2.6%;
larity 22.0%;
Conservative
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Kahn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ë
                                                                                                                                                                                                                                                                               Score 87; DB 21;
Pred. No. 8.20e+01;
33; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
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Pred. No. 8.20e+01
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Ā
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RESULTA
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CC (sic) +W200R substitution. It is encoded by BHK expression plasmid CC pM0N26451-4 (T59343). It is a specific example of the variant c-mpl CC ligands of the invention. The native c-mpl ligand is also referred to CC as Megakaryocyte Growth and Development Factor (MGDF) or thromobopoietin CC (TPO). Variants and chimera of c-mpl ligand can have an improved CC biological profile, such as increased activity and/or decreased side CC effects, and/or improved physical properties, such as improved half-life, cstability and/or stem cells, for the treatment of patients having a CC vivo expansion of stem cells, for the treatment of patients having a Sequence 332 AA;
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Best Local S
Matches 2
                                                                                                                                  06-DEC-1989.
02-JUN-1989; 870082.
03-JUN-1988; US-202271.
30-JUN-1989; AU-037256.
11-JUL-1989; MO-U02415.
N-PSDB; N92575.

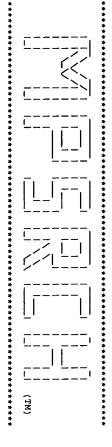
New recombinant DNA encoding HIV gag precursor protein - without flanking sequences, expressed in insect, yeast and mammalian cells, producing particles useful in vaccines and diagnosis Disclosure; Page 4-6; 17pp; French.

The inventors claim recombinant gag protein precursor (P93707) and
                                                                                                                                                                                                                        Sequence of the gag protein precursor. Vaccine; diagnosis; AIDS; LAV; HTLV-II Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Location/Qualifiers
misc_difference 281..300
/note= "encoded by T59343, missing from the sequence referred to in the specification"
                                                                                        (SMIK) SMITHKLINE Gheysen DA, Jacobs WPI; 89-358596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variant c-mpl ligand (1-332) P46L+W200R.

c-mpl ligand; Megakaryocyte Growth and bevelopment Factor; MGDF; thromobopoletin; TPO; variant; mutein; chimera; increased activity; decreased side effect; ex vivo expansion; stem cell; treatment; haematopoletic.disorder; gene therapy; human.
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                                                                                                                                                                                                              EP-345242-A.
                                                                                                                                                                                                                                                                                      P93707;
                                                                                                                                                                                                                                                                                                   T 15
P93707 standard; Protein; 504
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haematopoietic cells and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996; U00830.
03-FEB-1995; US-383035.
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08-AUG-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                       372
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                                                                                                                                                                                                                                                                                                                                                              431 HITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLA 465
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21; Conser
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larity 22.1%;
Conservative
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                                                                                                        BIOLOGIC.
E;
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No. 8.20e+01;
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Db 28 kyk-lkhivwasrelerfavnpglletsegcreilggl-gps1 68 : : : : : : :	CC the DNA encoding it (N92575) operatively linked to regulatory CC elements functional in eukaryotic cells. SQ Sequence 504 AA; Query Match 2.6%; Score 87; DB 3; Length 504; Best Local Similarity 37.2%; Pred. No. 8.20e+01; Matches 16; Conservative 12; Mismatches 10; Indels 5; Gaps 5;
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Colden AMETER 39 MAS SHI



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Jun 23 18:32:21 1998; MasPar time 23.69 Seconds 721.562 Million cell updates/sec

bular output not generated.

Title: >US-08-866-354-4 (1-468) from US08866354.pep 3384

Description: Perfect Score: Sequence: 1 MFLATLYFALPLIDLLMSAE......PVLMLTALAALLSVSLAETS 468

Scoring table: PAM 150 Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 46.167; Variance 82.676; scale 0.558

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 22																			ω	ພ	1	No. Score
92	90	93	90	90	91	92	91	90	91	92	94	94	96	96	95	99	00	103	102	801	178	;
	2.7																					Query Match
688	603	600	493	475	469	346	336	327	316	100	1186	857	826	769	169	352	522	399	249	397	24	Length
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C1HUS	S75664	S07638	JC5621	S49886	I37451	A70144	D70030	A55356	S58719	S26728	S72229	S33821	A60385	JC1121	I64089	S60024	S41819	S70983	898608	S70987	S69080	ID
complement subcompone	hypothetical protein	spore coat protein SP	epidermal growth fact	ā	2) P	hypothetical protein	alkanal monooxygenase	urokinase-type plasmi	probable membrane pro	hypothetical protein	meiotic recombination	median body protein -	surface an	leukocyte adhesion pr	4	bradykinin Bl recepto	52	dnaN protein - Mycoba	hypothetical protein	dnaN protein - Mycoba	glycosyl-phosphatidyl	Description
3.57e+00	6.45e+00					3.57e+00	4.80e+00	6.45e+00		3.57e+00	1.96e+00	1.96e+00	1.06e+00	1.06e+00	1.44e+00	4.17e-01	3.03e-01	1.16e-01	1.60e-01	.23e-	4.46e-14	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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acetolactate synthase	7	<pre>xotch protein - Afric</pre>	5	crumbs protein - frui	/ater di	leukocyte adhesion pr	leukocyte adhesion pr	probable regulatory p	env polyprotein - bab	_	æ	CDC1 protein - yeast	n facto	probable histidine pr	carboxypept1dase B (E	LPS biosynthesis RfbU	leukosialin precursor	neurogenic repetitive	probable membrane pro	hypothetical protein	integrin beta 2 chain
2.03e+01	2.03e+01	8.63e+00	٠	1.53e+01		8.63e+00	•	•	8.63e+00	1.53e+01	1.15e+01	8.63e+00	1.53e+01	1.15e+01	1.15e+01	1.53e+01	1.15e+01	1.53e+01		2.65e+00	

#journal #title #ccession	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors	Query Match Best Local Simi Matches 24; Db 1 MFLATLY Qy 1 MFLATLY	# # Journal Natu: # # # # # # # # # # # # # # # # # # #	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors
Cole, S.T.; Takiii, H.E. Mol. Microbiol. (1996) 20:283-293 Organization of the origins of replication of the chromosomes of Mycobacterium smegmatis, Mycobacterium leprae and Mycobacterium tuberculosis and isolation of a functional origin from M. smegmatis.	\$70987 #type complete dnaw protein - Mycobacterium smegmatis #formal_name Mycobacterium smegmatis 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Mar-1998 \$70987 \$70980 \$70980 \$30980 \$70980 \$70980 \$70980 \$70980 \$70980 \$70980	tch 5.3%; Score 178; DB 2; Length 24; al Similarity 100.0%; Pred. No. 4.46e-14; 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MFLATLYFALPLLDLLMSAEVSGG 24	POLISEN, K.T.; BECK, C.D.; Gray, C.; Armanini, M.F.; POLIOCK, R.A.; Hefti, F.; Phillips, H.S.; Goddard, A.; MOORE, M.W.; Buj-Bello, A.; Davies, A.M.; Asai, N.; MACHARASHI, M.; Vandlen, R.; Henderson, C.E.; Rosenthal, A. Nature (1996) 382:80-83 Characterization of a multicomponent receptor for GDNF. S69080 S69080 Preliminary type mRNA 1-24 ##label TRE 1-24 ##label TRE	

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Best Local Similarity 25.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                   Matches
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#title Analysis of the protein-coding content of the sequence human cytomegalovirus strain AD169.
#cross-references MUID:90269039
                                      #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-249 ##label CHE
##cross-references EMBL:X17403; NID:g59591; PID:g1780882
##note this sequence was submitted to the EMBL Data
December 1989
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##cross-references EMBL:x92503
##note the nucleotide
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Local Similarity 38.3%;
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GTG
                                                                                                           #type complete
dnaN protein - Mycobacterium tuberculosis
#formal_name Mycobacterium tuberculosis
12-Feb-1998 #sequence revision 20-25-5
Salazar, L.; Fsihi, H.; de Rossi,
Cole, S.T.; Takiff, H.E.
Mol. Microbiol. (1996) 20:283-293
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07-Sep-1990 #sequence_revision
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translation not shown
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11 protein UL103 -
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Pred. No. 2.23e-02;
27; Mismatches 50; Indels
                  de Rossi,
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Kouzarides,
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                                                                                                                                                                                                                                                                                                                             ##residues 1-417,'RA',420-430,'Q',432-506,'V',508-522 ##label
##cross-references EMBL:X58521; NID:g432653; PID:g432654
#length 522 #molecular-weight 53268 #checksum 4396
                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
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##cross-references EMBL:X58521
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##note the nucleotide sequence was
Library, October 1995
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##residues 1-399 ##label SAL
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                                                                 $60024 #type complete
bradykinin B1 receptor - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hurt, E.C.
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Eur. J. Cell Biol. (1991) 55:17-30
Human nucleoporin p62 and the essential yeast nuclear pore
protein NSP1 show sequence homology and a similar domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S41819 #type complete
nucleoporin p62 - human
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995
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Pred. No. 3.03e-01
19; Mismatches 1
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Pred. No. 1.16e-01;
27; Mismatches 42; Indels
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KEYWORDS
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REFERENCE
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Best Local
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Best Local
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-169 ##label TIGR
##cross-references GB:U32758; GB:L42023; NID:g1573747; PID:g1573750;
TIGR:HI0743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AILFFNCHILA-SLRRRGERVPSRCG-GPRD-SKSTALILTLVASFLVCWAPYHFFAFLE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-352 ##label MAC ##cross-references EMBL:U20507; NID:g1041820; PID:g1041821 ##cross-references EMBL:U20507; NID:g1041820; PID:g1041821 ##cross-references EMBL:U20507; NID:g1041820; PID:g1041821 ##cross-references EMBL:U20507; NID:g1041820; PID:g1041821 ##cross-references EMBL:U20507; NID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041820; PID:g1041821; PID:g1041820; PID:g1041820; PID:g1041821; PID:g1041820; PID:g1041821; PID:g1041820; PID:g1041821; PID:g1041821; PID:g1041820; PID:g1041821; PID:g1041820; PID:g1041821; PID:g1041821; PID:g1041820; PID:g1041821; PID:g1041821;
        245
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                                                                                  74 TLEDSGDVAFICEVKQAGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLV 127
        SLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYS-GLIGTVM 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 2.9%;
Similarity 25.0%;
25; Conservative
                                                                                                                                                                         14;
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Mezrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
                                                                                                                                                                                                                                                                                                                                                                                                                one of the proteins required for the normal export of envelope proteins out of the cell cytoplasm; may be involved in the initiation of the exporting process #superfamily protein-export protein secB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MacNell, T.: Bierilo, K.K.: Menke, J.G.: Hess, J.F.
Biochim. Biophys. Acta (1995) 1264:223-228
Cloning and pharmacological characterization of a rabbit
bradykinin B(1) receptor.
                                                                                                                                                                                                                                                                                                                                          protein export
#length 169 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole-genome random sequencing and assembly of Haemophilus influenzae {\tt Rd}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Haemophilus influenzae 18-Aug-1995 #sequence_revision 18-Au
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                                                                                                                                                                                                                2.8%;
25.9%;
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                                                                                                                                                                                                                                                                                                                                      #molecular-weight 19132 #checksum 8441
                                                                                                                                                                                                                Score 95;
Pred. No.
                                                                                                                                                                         Pred.
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Pred. No. 4.17e-01;
35; Mismatches 30; Indels
                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                       Length 169
                                                                                                                                                                     Indels
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RESULT

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REFERENCE
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                          RESULT
##residues 1-826 ##label YOS
##cross-references EMBL:X13335
CLASSIFICATION #superfamily disintegrin
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445-631
701-723
724-769
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#journal
#title
                                                                                                                                                             #journal #title
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642
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#accession JC1121
                                                                                             #accession
                                                                                                                                                                                                                               #authors
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WT The leukocyte adhesion proteins are noncovalently linked
heterodimers of distinct alpha and identical beta chains. These
structurally related glycoproteins mediate cell-adhesion
reactions, and a deficiency of them is attributed to a genetic
defect in the expression or structure of their common beta chain.
GEICATION *superfamily integrin beta chain.
cell adhesion; cytoskeleton; duplication; glycoprotein;
heterodimer; leukocyte; pyroglutamic acid; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 IGKNCECQTQGRSSQELEGSCRKDNSS-II-CS-GLGDCICGQCVCHTS----D-VPNK 527
                                              ##molecule_type mRNA
##residues 1-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 KIYGQ-FCECDNVNC-ER 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 ISKGNNCLDAAKAC-NLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 HSYGMLFCSCRDIACTER 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukocyte adhésion protein beta chain precursor - bovine
surface glycoprotein CD18
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                                                                                                            Int. Immunol. (1990) 2:585-591
Molecular cloning of cDNA encoding MS2 antigen, a novel of surface antigen strongly expressed in murine monocytic lineage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of the bovine CD18-encoding the human and murine glycoproteins.
                                                                                             A60385
                                                                                                                                                                                                                                                                                                                   monocyte surface antigen MS2 precursor - mouse #formal_name Mus musculus #common_name house mouse 03-Feb-1993 #text_change
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Gene (1992)
                                                                                                                                                                                                                            Yoshida, S.;
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                                                                                                                                                                                                         Yamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#product leukocyte adhesion protein beta chain #statu
predicted #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #binding_site carbohydrate (Asn) (covalent) #status
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#domain intracellular #status predicted #label CYT\
#modified_site pyrrolidone carboxylic acid (Gln) (if
mature form) #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain extracellular #status predicted #label EXT\
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92) 114:267-271
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  homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.T.; Kehrli Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta chain precursor - bovine
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                                                                                                                                                                                                                               Akizuki,
                                                                                                                                                               a novel cell
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ACCESSIONS
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Best Local Similarity 31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 ELVLQGTKC-EEGKVC-MDGSCQDLR-VYRSENCSAKCNNHGVCNHKRECH 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-857 ##label MAR
##cross-references EMBL:X64517; NID:g312670; PID:g312671
##cross-references EMBL:X64517; NID:g312670; PID:g312671
                                                                                                                                  ##residues 1-1186 ##label MCK
##cross-references EMBL:U35631; NID:g1017733; PID:g1017734
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2.8%;
Similarity 27.0%;
20; Conservet
                                                                   me1-218
45/2; 558/3;
#length 1186
                                                                                                                                                                                                                         Cloning of the Drosophila melanogaster meiotic recombination gene mei-218: a genetic and molecular analysis of interval 15E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marshall, J.; Holberton, D.V.
J. Mol. Biol. (1993) 231:521-530
Sequence and structure of a new coiled
microtubule bundle in Giardia.
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#domain disintegrin homology #label DIS\
#domain transmembrane #status predicted #label TMM\
#active_site Glu #status predicted
#length 826 #molecular-weight 89896 #checksum 2686
                                                                                                                                                                                                                                                                        McKim, K.S.; Dahmus, J.B.; Hawley, R.S. Genetics (1996) 144:215-228
                                                                                                                                                                                                                                                                                                                                                         #formal_name Drosophila melanogaster
04-Feb-1998 #sequence_revision 13-Feb-1998
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                                                                   #molecular-weight 133551
   Score 94; DB 2; Length 1186; Pred. No. 1.96e+00; 23; Mismatches 25; Indels
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Pred. No. 1.96e+00,
16; Mismatches 1:
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Pred. No. 1.06e+00
12; Mismatches 1
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                                                         ##cross-references EMBL:Z71334; NID:g1301928;
                                                                       ##molecule_type DNA
##residues 1-316 ##label BEW
                                                                                                                                                                                        ##residues 1-316 ##label BER
##cross-references EMBL:U12141; MID:g1314216; PID:g994828
##cross-reference EMBL:U121416; PID:g994828
##cross-reference EMBL:U12141; PID:g994828
##note was submitted to 1
Library, July 1994
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the nucleotide sequence was
#inote thibrary, September 1992
y #length 100 #checksum 201
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Similarity 31.5%;
17; Conservation
                                                                                                              Bergez, P.; Do
submitted to
S62986
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hypothetical protein 100-plus (rpoA2 3' region) -
Thermoplasma acidophilum (fragment)
#formal_name Thermoplasma acidophilum
12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                          Bergez, P.; Dolgnon, F.; Crouzet, M. Yeast (1995) 11:967-974
The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV from Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein N2433; hypothetical
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   cerevisiae)
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16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change
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                                                                                                                                                                                                                                                                                     nucleic acid sequence
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                                       MIPS:YNL058c
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o the Protein
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                                                                                                                                Crouzet,
Sequence
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Database,
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                                                         PID:e239896; PID:g1301929;
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Best Local Similarity 28.6%;
Matches 18; Conservative
                                                                                                                                     Query Match 2.7%;
Best Local Similarity 24.2%;
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117-205
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32,75,183,193,221,
254,282
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250
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##cross-references GB:U12235; NID:g555809; PID:g555810
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                                     233 CSYEERERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYSGL 292
                                                                          192 CNYTHCNGGPVLDLQSFPPNGFQCYSCEGNNTLGCSSEEASLINC-RGPMNQCLVA-TGL 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
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#formal_name Mus musculus #common_name house mouse
06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                         *superfamily urokinase-type plasminogen activator Ly-6 homology alternative splicing; duplication; glycoprotein; phosphatidylinositol linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kristensen, P., Eriksen, J., Blasi, F., Dano, K.
J. Cell Biol. (1991) 115:1763-1771
Two alternatively spliced mouse urokinase receptor mRNAs with different histological localization in the gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suh, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
J. Biol. Chem. (1994) 269:25992-25998
The murine urokinase-type plasminogen activator receptor
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precursor - mouse
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                                                                                                                  Conservative
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gth 316
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                                                                                                                                                                                                                                    *binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                          #domain Ly-6 homology #label 1LY6\
#domain Ly-6 homology #label 2LY6\
#domain Ly-6 homology #label 3LY6\
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h 327 #mol
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#molecular-weight 35046 #checksum 6749
                                                                                                                Score 90; DB 2; Length 327; Pred. No. 6.45e+00; 22; Mismatches 46; Indels
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Pred. No. 4.80e+00;
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TITLE
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REFERENCE
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CLASSIFICATION
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                                                                   132 NSGEDFPEQLEELRNYFKPSGNVRNQVRAIPGEGIDVPIW 171
                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-336 ##label KUN
##experimental_source strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status
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                                                                                                                                                                      Match 2.7%;
Local Similarity 40.0%;
       NSGNDLEDCLKFL-NFFKDNTCLKNAIQAF-GNGSDVTMW
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                         #superfamily ynbW protein
#length 336 #molecular-weight 37101 #checksum
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                                                                                                                                      Conservative
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A.; Braun, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation not shown
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                                                                                                                                      12;
                                                                                                                                                                      Score 91; DB 2; I
Pred. No. 4.80e+00;
                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moszer, I.; Albertini, A.M.;
Bertero, M.G.; Bessieres, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence not shown;
                                                                                                                                                                                                         Length 336
                                                                                                                                             Indels
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Search completed: Tue Jun Job time : 121 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Tue Jun 23 18:28:42 1998; MasPar time 16.07 Seconds 730.390 Million cell updates/seconlar output not generated.

Title: >US-08-866-354-4
Description: (1-468) from USO8866354.pep
Perfect Score: 3384
Sequence: 1 MFLATLYFALPLLDLLMSAE.......PVLMLTALAALLSVSLAETS 468
Scoring table: PAM 150
Gap 11
Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 47.975; Variance 67.645; scale 0.709

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4 4 5 4	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24
. 8 8	88	88	89	88	88	89	87	88	87	88	89	88	88	89	93	93	92	93	93	91
N N 6 6	2.6	2 6	2.6	2 6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7
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NTC3_MOUSE	HAP1_HAEIN	PPSA_METJA	ITB2_MOUSE	ITB2_PIG	STB5_YEAST	ENV_BAEVM	NU62_RAT	GAG_HV2SB	GUXC_FUSOX	GAG_HV1MN	CC1_YEAST	CBPB_RAT	LEUK_RAT	SUMT_PSEFL	HEPA_HCMVA	CASP_MESAU	C1S_HUMAN	SP96_DICDI	CHI3_CANAL	GAG_HV1JR
NEUROGENIC LOCUS NOTCH	ADHESION AND PENETRATI	PROBABLE PHOSPHOENOLPY	CELL SURFACE ADHESION	CELL SURFACE ADHESION	STB5 PROTEIN.	ENV POLYPROTEIN PRECUR	NUCLEAR PORE GLYCOPROT	GAG POLYPROTEIN (CORE	PUTATIVE EXOGLUCANASE	GAG POLYPROTEIN (CONTA	CELL DIVISION CONTROL	CARBOXYPEPTIDASE B PRE	LEUKOSIALIN PRECURSOR	UROPORPHYRIN-III C-MET	DNA HELICASE/PRIMASE C	CALCIUM-DEPENDENT SERI	COMPLEMENT C1S COMPONE	SPORE COAT PROTEIN SP9	CHITINASE 3 PRECURSOR	GAG POLYPROTEIN (CONTA
2.29e+00 1.62e+00	2.29e+00	2.29e+00	1.62e+00	2.29e+00	2.29e+00	1.62e+00	3.22e+00	2.29e+00	3.22e+00	2.29e+00	1.62e+00	2.29e+00	2.29e+00	1.62e+00	3.88e-01	3.88e-01	5.57e-01	3.88e-01	3.88e-01	7.97e-01

ALIGNMENTS

Query Ma Best Loc Matches	DR EMBL: UD R RECEPTOR SIGNAL FT CHAIN FT PROPEP FT DOMAIN FT CARBOHYD FT CARBOHYD SQ SEQUENCE	SEQU TISS MEDL JING ANTO FOX CELL	i C
/ Match Local Similarity nes 468; Conse	VD VD VD CE	IL) SEQUENCE FROM N.A. TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; JING S., WEN D., YU Y., JING S., WEN D., YU Y., ANTONIO L., HU Z., CUPPL FOX G.M.; CELL 85:1113-1124(1996). FOUNCTION: RECEPTOR F AUTOPHOSPHORYLATION AUTOPHOSPHORYLATION -I- SUBURIT: 2 MOLECULES WITH THE DISULFIDE-L -I- SUBCELLULAR LOCATION: -I- TISSUE SPECIFICITY: -I- SIMILARITY: BELONGS	GDNF L STANN Q62997; Q62997; Q1-NOV-1997 (REL. 3: Q1-NOV-1997 (REL. 3: Q1-NOV-1997 (REL. 3: Q1-NOV-1997 (REL. 3: QNF RECEPTOR ALPHA NEUROTROPHIC PACTOR RECTOR TRNR1 RECTOR OR TENR1 RECTOR ORVEGICUS (I EUTHERIA; RODENTIA.
100.0%; arity 100.0%; Conservative	4	IL) SEQUENCE FROM N.A. TISSUE-RETINA; TISSUE-RETINA; JING S., WEN D., YU Y., HOLST ANTONIO L., HU Z., CUPPLES R., FOX G.M.; CELL 85:1113-1124(1996). FOX G.M.; FOX G.M	TANI 31. 31. 32. 33. 34. 37. 37. 37. 37. 37. 37. 37. 37. 37. 37
; Score ; Pred. 0; N	PI-ANCHOJ POTEL GDNF HYDR (POTL) POLY POTEL POTEL POTEL POTEL POTEL POTEL POTEL	IL) SEQUENCE FROM N.A. TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE=RETINA; TISSUE-RETINA; TISSUE-RETINA; TISSUE SECONDANIA P.L., LOUIS JC., HU S., ALTROCK B.1 FOX G.M.; TISSUE SECONDANIA P.L., LOUIS JC., HU S., ALTROCK B.1 FOX G.M.; TOUTON RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED FUNCTION: RECEPTOR. AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTORI- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULESI- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-AI- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEYI- SIMILARITY: BELONGS TO THE GDNFR FAMILY.	ARD; PRT; 468 AA. CREATED) LAST SEQUENCE UPDATE) PRECURSOR (GDNFR-ALPHA) (TGF-BETA RECEPTOR 1). RAT). CHORDATA; VERTEBRATA; TETRAPODA; 1
3384; DB 1; No. 0.00e+00; Mismatches 0	NCHOR; MEMBRANE; SIG POTENTIAL. GEONE RECEPTOR ALPHA. HYDROPHOBIC, REMOVEL (POTENTIAL). POLY-THR. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.	P.L., LUO Y., F. LOUIS JC., H LOUIS JC., H F. MEDIATES THE F. MEDIATES THE F. MEDIATES THE GIONE DIMER AND 10 GONE DIMER AND 10 CHED TO THE MEM SED IN LIVER, B GDNER FAMILY.	PRT; 468 AA.)) QUENCE UPDATE) NOTATION UPDATE (GDNFR-ALPHA) 1). VERTEBRATA; TE:
1; Length 468; +00; 0; Indels	. ALPHA. REMOVED DURING	HUS., ALTROCK B. HUS., ALTROCK B. IE GDNF-INDUCED IE RET RECEPTOR. THOUGHT TO FORM A DWITH 2 MOLECULES MBRANE BY A GPI-A BRAIN AND KIDNEY	AA. E) ATE) A) (TGF·BETA RELATED A) TETRAPODA; MAMMALIA)
0;	ING MATURATION	ES BR	RELATED VAMMALIA;
Gaps 0;	VTION	COMPLEX OF RET.	

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                                                                     Matches
                                                                                                                                                        DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                      RECEPTOR;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDNR_MOUSE STANDARD; PRT; 468 AA.
p97785;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA
NEUROTROPHIC FACTOR RECEPTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-DORSAL ROOT GANGLION;
                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNFRA OR TRNR1
                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WATABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                          Local
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                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
L; AB000800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
MFLATLYFVLPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS 468
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                                                                     456; Conser
                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE;
1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  BELONGS TO THE GDNFR FAMILY. G1816442; -.
                                                                                                                                                                                                                            369
59
                                                                                                                                                                                                                                                                                             468
                                                                                        98.6%;
                                                                                                                                                           51782
                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTACHED TO THE MEMBRANE
                                                                                                                                                    HYDROPHOBIC, REMOV
(POTENTIAL).
POLY THR.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                        Score 3335; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                               GDNF RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETRAPODA;
                                                                                                                                                                                                                                                                                             REMOVED DURING
                                                                2
                                                                                                            Length
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВУ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPI-ANCHOR
                                                                                                                                                                                                                                                                                             MATURATION
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RESERVATION OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNR_HUMAN
P56159;
01-NOV-1997
                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) ('NEUROTROPHIC FACTOR RECEPTOR 1).
GDNFRA OR TRNR1.
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
JING S.,
                                                                                                                                                                        SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     CELL 85:1113-1124(1996).
-:- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE AUTOPHOSPHORYLATION AND ACTIVATION OF THE
                                  SEQUENCE
                                                                                                                  DOMAIN
                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: ATTACHED SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GDNE
                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                           FOX G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-SUBSTANTIA NIGRA;
MEDLINE; 96270513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA;
                                                                                                                                                                                                              RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTONIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
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                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SUBUNIT: 2 MOLECULES OF GD
WITH THE DISULFIDE-LINKED
                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTTTAMTTTAFRIKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEN D., YU Y.,
L., HU Z., CUPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIMATES
                                                                                                                                                                                                              GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAZOA;
                                                                                                                                                        25
7
                                                                                                                                                                                                                                                                                                                           MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX ISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUPPLES R., I
                                                                          368
59
346
                                                                                                                                                        464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHORDATA; VERTEBRATA;
  94.28;
                                                                                                                                                                                                              GPI-ANCHOR; MEMBRANE;
                                      MW;
                                                                                                                                                                                                                                                     THE GDNFR FAMILY.
                                                      HYDROPHOBIC, I
(POTENTIAL).
POLY-THR.
POTENTIAL.
POTENTIAL.
POTENTIAL.
Score
                                                                                                                                            GDNF RECEPTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.L., I
                                      2C8C3574
3187;
                                                                                                                                                                                                                                                                                         TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             :S J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464
                                    CRC32;
B
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                                                                                                                                                                                                                                                                                         MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FANG M., TAMIR
HU S., ALTROCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TGF-BETA
                                                                                                                                                                                                                                                                                                                                                                                     GDNF-INDUCED
RET RECEPTOR
                                                                                                                                                                                                              SIGNAL
Length 464;
                                                                                                                                                        DURING
                                                                                                                                                                                                                                                                                         ВΥ
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                                                                                                                                                                                                                                                                                           GPI - ANCHOR
                                                                                                                                                        MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. W.
                                                                                                                                                                                                                                                                                                                                                                                       (BY
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Query Match

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RESULT
AC CO.
DT CO.
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olinov-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BUJ-BELLO A., ADU J., PINON L.G., HORTON A., THOMPSON J.,

ROSENTHALA A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;

NATURE 397:721-724(1997).

-I- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCE

AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTC
DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                 RECEPTOR;
SIGNAL
                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                  SIMILARITY:
L; U90541; G:
                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE WITH THE DISULFIDE-LINKED GDNF DIMER AND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ATTACHED TO THE
                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNCL-LQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGTVMTPN 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEPVNSRLSDIFRVVPFISDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTT 180
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                                                                                                                                                                                                              GLYCOPROTEIN;
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405
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G2213803;
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368
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346
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                                                                                                                                                          469
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                                                                                                                                                                                                                                       GPI-ANCHOR; MEMBRANE;
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                                                                                                                           GDNF RECEPTOR ALPHA HYDROPHOBIC, REMOVE (POTENTIAL).
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                                                                                                                                                                                                                                                                                           GDNFR FAMILY.
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Mismatches 4;
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                                                                                                                                                               REMOVED
                                                                                                                                                                                                                                                                                                                                               MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                              THOUGHT D WITH 2
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RET RECEPTOR
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                                                                                                                                                               MATURATION
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Best Local S
Matches 36
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000451;
01-NOV-1997
                                                                                                     SIGNAL
CHAIN
                                                                                                                                                                                  EMBL;
  CARBOHYD
                                                    PROPEP
                                                                                                                                                            RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GDNFR-BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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                                                                                                                                                                                        601956;
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S
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MEDLINE: 97325791.
BALOH R.H., TANSEY M.G., GOLE
HEUCKEROTH R.O., KECK C.L., 2
JOHNSON E.M., MILBRANDT J.;
NEURON 18:793-802(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 3:
01-NOV-1997 (REL. 3:
01-NOV-1997 (REL. 3:
NEURTURIN RECEPTOR A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                           -!- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                         GDNFRB OR TRNR2
                                                                                                                                                                                                                                                                                                                                                                                                                       BETA RELATED NEUROTROPHIC
                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPNYIDSSSLSVAPWCDCSNSGNDIDECRKFLNFFQDNTCLKNAIQAFGNGTDVNVWQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REKPNCLNLQESCKKNYICRSRLADFFTNCQPESRSVSSCLKENYADCLLAYSGLIGTVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSDFGKDGLAGAS-SHITTKSMAAPPSCSLSSLP-VLMLTALAALLSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NENAIGKONTPGVSTSHISSENSFALPTSFYPSTPLILMTIALSLFLFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYSGLIGTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
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                                                                                                                          MILARITY: BELONGS TO
AF002700; G2145080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 76.8%;
Similarity 78.1%;
367; Conservative
                                                                                                                                                                                                                                                                                                                                        PRIMATES.
                                                                                                 GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469
 52
                                                                                                                                                                                                                                                                                                                                                                                                L. 35, CREATED)

L. 35, LAST SEQUENCE UPDATE)

JL. 35, LAST ANNOTATION UPDATE)

PTOR ALPHA PRECURSOR (WINE-ALPHA) (NRTN

PTOR ALPHA PRECUPSOR (PTOR 2) (GDNE RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                            464
                                                                                                                                                                                                                                                                                                                                                        CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52043 MW;
 52
                                                                              GPI-ANCHOR; MEN
POTENTIAL.
                                                                                                                                                                                                                                                          GOLDEN J.P., CREEDON D.J.
L., ZIMONJIC D.B., POPESCU
                                                                                                                                            THE GDNFR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2598; DB 1;
Pred. No. 0.00e+00;
49; Mismatches 41
(POTENTIAL).
                               HYDROPHOBIC,
                                                  TGF-BETA RELATED RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8D241C9 CRC32;
                                                                                             MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464
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                               REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                         TETRAPODA; MAMMALIA;
                                                               NEUROTROPHIC
                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (NRTNR-ALPHA)
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                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464
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                                                                 FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                    NRTR_MOUSE
008842;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 97325791.

BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
HEUCKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
JOHNSON E.M., MILBRANDT J.;
MEURON 18:793-802(1997).
PUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.

-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCH
                                                                                                                                                                                                                                                                   00864;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA) (NRTNR-ALPHA) (TGF-
                                                                                                                                                                                                                                                    (GDNFR-BETA).
GDNFRB OR TRNR2.
MUS MUSCULUS (MC
            PROPER
                                   CHAIN
                                                         RECEPTOR;
                                                                       EMBL;
                                                                                                                                                                                                                            EUTHERIA;
                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                     SIMILARITY: BELONGS TO THE GDNFR FAMILY. L; AF002701; G2145082; -
                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REISPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYEDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLDETLRSLASPSSLQGPELHGWRPPVDCVRANELCAAESNCSSRYRTLRQCLAGRDRN-
                                                                                                                                                                                                                                                                                                                                                                                                         DSDFGKDGLAGASSHITTKS-MA-APPSCSLSSLPVLMLT-AL
                                                                                                                                                                                                                                                                                                                                                                                                                               E--LTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLKQAL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPYQTTTATTTTAFRYKNKPLGPAGSENEIPTHYLPPCANLQAQKLKSNVSGSTHLCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNYVDSS-S-LSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNYVDSSFTGIVVSPWCSCRGSGNMEEECEKFLRDFTENPCLRNAIQAFGNGTDVNVSPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLGSYAGMIGFDMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
224; Conse
                                                         GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE;
                                                                                                                                                                                                                              RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
413
464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.0%;
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413
51558
            463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1556;
Pred. No. 0.
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POTENTIAL.
3C74BBFB CRC32;
                      POTENTIAL.
TGF-BETA RELATED NEUROTROPHIC RECEPTOR 2.
HYDROPHOBIC, (POTENTIAL).
                                                                                                                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                           463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00e+00;
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                                                                                                                                                                                                                                       TETRAPODA;
            REMOVED
                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                         456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
            DURING
                                                                                                        BY A GPI-ANCHOR
                                                                                                                                                                                                                                       MAMMALIA;
            MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                   FACTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        416
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CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                 NRTR_CHICK STANDARD; PRT; 465 AA 013157; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT) NEURTURIN RECEPTOR ALPHA PRECURSOR (NTNR-AL)
                                           SIGNAL
CHAIN
                                                                      EMBL;
                                                                                                -!- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                         BUJ-BELLO A., ADU J., PINON L.G., HORTON A., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., D NATURE 387:721-724(1997).
                                                                                                                                                                                         GDNFRB.
GALLUS GALLUS
                                                                                                                                                                                                           RECEPTOR BETA) (GDNFR-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                   PROPEP
                                                             RECEPTOR;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                       GALLIFORMES
                                                                                                                                                                               EUKARYOTA;
                                                                               -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                  442
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                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                           STALTALPLLMVT-LA 463
                                                                                                                                                                                                                                                                                                                                              DSTS-LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVIKLYSGSCRARL | : : | | : : : | ; : : | ; : : | ;
                                                                                                                                                                                                                                                                                                                                                                                 EEECEKFLKDETENPCLRNAIQAFGNGTDVNM-SPKGPTFSATQAPRVE-KTPSLPDDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                          | :|::||:||:| ||
SCSLSSLPVLMLTALA
                                                                                                                                                                                                                                                                                                                                    GSENEIPTHYLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCRCKRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGAD
                                                                                                                                                                                                                                                                                                                                                                        LEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPA
                                                                      U90542; G2213805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity
214; Conser
                                                             GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
357
413
463
                                                                                                                                                                               METAZOA;
355
387
412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                         (CHICKEN)
                                                                               BELONGS
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357
413
51598 ,
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49.1%;
 355
387
412
                                   465
                                                                                                                                                                               CHORDATA;
                                                                                                                                                                                                                                                                                                  457
                                                              GPI-ANCHOR;
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W.
                                                                               THE GDNFR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1539; DB 1;
Pred. No. 0.00e+00;
96; Mismatches 113
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                          NEURTURIN RECEPTOR ALPHA HYDROPHOBIC, REMOVED DUR: (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                      POTENTIAL.
                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0A2165C0
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                                                                                                                                                                                                                  ION UPDATE)
(NTNR-ALPHA) (NRTNR-ALPHA)
                                                             MEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32
                                                                                                                                                                                TETRAPODA;
                                                                                                                                   DAVIES A.M.
                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                    DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                AVES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463;
                                    MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                NEOGNATHAE
                                                                                                                                                                                                                   (GDNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                             SALAZAR L., FSIHI H., DE ROSSI E., RICCARDI G., RIOS C.,

A COLE S.T., TAKIFF H.E.;

AL MOL. MICROBIOL. 20:283-293(1996).

**COLE S.T., TAKIFF H.E.;

**MOL. MICROBIOL. 20:283-293(1996).

**COLE S.T., TAKIFF H.E.;

**MOL. MICROBIOL. 20:283-293(1996).

**COLE S.T., TAKIFF H.E.;

**MOL. MICROBIOL. 20:283-293(1996).

**COLE S.T., TAKIFF H.E.;

**C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEGUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DNA POLYMERASE III, BETA CHAIN (EC 2.7.7.7).
EMBL; X92503; E208988; -.
DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION
SEQUENCE 397 AA; 41324 MW; EFFB3064 CRC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOBACTERIUM SMEGMATIS. PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96310367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CS--LSSLPVLMLTAL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EECEKFLRDFTENPCLRNAIQAFGNGTDVNL-SPKNPSPPITMLPKVE-KSPALPDDIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKHSYGMLFCSCRDIACTERRRQTIVPVCSYEERERPNCLSLQDSCKTNYICRSRLADFF 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRCKRGMRKEIQCLQVYWSIHLGLAEGEEFYEASPYEPITSRLSDIFRLASIFSGM-DPA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENEIPTHYLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPS
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203; Conser
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larity 46.6%;
Conservative
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102; |
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Pred. No. 0.00e+00;
102; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5CA073E4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AA
  CRC32;
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Query Match
Best Local Similarity
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Best Local
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P16734;
                                                                                                                                                                                                                                                                                                                                                                                 NU62_HUMAN
P37198;
                                                                                                                    SEQUENCE FROM N.A.

MEDLLINE; 92007939.

CARMO-FONSEGA M., KERN H., HURT E.C.;

EUR. J. CELL BIOL. 55:17-30(1991).

-i- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEAR PORE COMPLEX.

THE N-TERMINAL IS PROBABLY INVOLVED IN NUCLEOCYTOPLASMIC

TRANSPORT. THE C-TERMINAL IS PROBABLY INVOLVED IN PROTEIN-PROTEIN

INTERACTION VIA COILED-COIL FORMATION AND MAY FUNCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHV-1 55, VZV 53, EBV BBRF2, HCMV UL103 AND EMBL; X17403; G59711; -.
PIR; S09868; S09868.
SEQUENCE 249 AA; 28636 MW; 239ADB2D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R., HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTICHETTI J.A., PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B. CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).

-I- SHMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UI
01-APR-1993 (REL. 25, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62).
                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                        NUP62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
                                                                                                                                                                                                                                                            EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 90269039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN UL103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 ESVVLAATDRFRLAVRELTWYTTAGDVEAAVLVPAKTL-AEAAKAGTDGNQVHLALGSGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 DFGKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 SVGKDGLLGIRSE-GKRSTTRLLDAEFPKFRQLLPAEHTAVATIGVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 27; Conser
              ANCHORAGE OF P62 TO THE PORE COMPLEX.
SUBCELLULAR LOCATION: CENTRAL REGION
THE TRANSPORTER. DURING MITOTIC CELL
THE POLES OF THE MITOTIC SPINDLE.
DOMAIN: CONTAINS X-F-X-F-G REPEATS.
PTM: O-GLYCOSYLATED. CONTAINS ABOUT 1
CHAIN SITES PREDICTED FOR THE ENTIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTVISCVENCNLTRKCLHDLLQYLDAVNVRESFGRLLHHSARRLICS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTSMSNEVCN-RRKCHKALRQFFDKVPAKHSYG-MLFCSCRDIACT
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    THE C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.3%;
                                                                                                                                                                                                                                                                            CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102; DB 1;
Pred. No. 1.28e-02;
7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 1;
Pred. No. 1.15e-03;
27; Mismatches 50
                                                                                                                                                                                                                                                                            VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                 ABOUT 10 N-ACETYLGLUSAMINE SIDE ENTIRE PROTEIN, AMONGST WHICH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON UPDATE)
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                                                                             OF THE NUCLEAR PORE, WITHIN DIVISION, IT ASSOCIATES WITH
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7 R
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Best Local
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P48748;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
CARBOHYD
SEQUENCE
                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEPTOR; FALSE_NEG.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                          -I- FUNCTION: THIS IS A RECEPTOR FOR BRADYKININ. COULD CHRONIC PAIN AND INFLAMMATION.
-I- SUBCELLULAR LOCATION: INFEGRAL MEMBRANE PROTEIN.
-I- INDUCTION: THE B1 RECEPTOR IS SYNTHESIZED DE NOVO I
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NEW ZEALAND WHITE; TISSUE-AORTA;
MEDLINE; 96085127.
MACNEIL T., BIERILO K.K., MENKE J.G., HESS J.F.;
BIOCHIM, BIOPHYS, ACTA 1264:223-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORYCTOLAGUS CUNICULUS (RABBIT) EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
B1 BRADYKININ RECEPTOR (BK-1 RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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REPEAT
                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                       - I - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; LAGOMORPHA.
   DOMAIN
                     TRANSMEM
                                                                             DOMAIN
                                                                                               TRANSMEM
                                                                                                                                    TRANSMEM
                                                                                                                                                        DOMAIN
                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3DKRB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: HIGH, WITH RAT P62 NUCLEOPORIN. SIMILAR N-TERMINAL REPEAT ORGANIZATION WITH CENTRAL REPEATING UNITS OF YEAST NSP1, X58521; G432654; -.
                                                                                                                                                                                                                                                                                                          TISSUE INJURY.
                                                                                                                                                                                                                                                                         U20507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 3.0%;
Similarity 31.6%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN;
PALMITATE.
1 39
40 64 72
73 97
98 110
111 132
133 154
177
175 198
199 225
226 246
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                                                                                                                                                                                                                                                                   G1041821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468
53321
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11.
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13.
14.
15.
COILED COIL.
GLNAC (BY SIMILARITY).
GLNAC (BY SIMILARITY).
                                                                       EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 1;
Pred. No. 2.80e-02;
19; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOPROTEIN; HEPTAD REPEAT PATTERN;
4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCEOACA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X 9 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 522;
                                                                                                                                                                                                                                                                                                                              NOVO IN RESPONSE
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                                                                                                                                                                                                                                                                                           RECEPTORS
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1

RESULT 13 ID GAG_HV1MA

STANDARD;

PRT;

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RESULT ACCORDED TO THE SECOND 
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Best Local S
Matches 2
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
LIPID
                                                                                                                                                                                                                                                                                                                   SCIENCE 269:496-512(1995).

-I- FUNCTION: THIS IS ONE OF THE PROTEINS REQUIRED FOR THE NORM EXPORT OF ENVELOPE PROTEINS OUT OF THE CELL CYTOPLASM; IT MEDITOR OF THE EXPORTING PROCESS, BY BE INVOLVED IN THE INITIATION OF THE EXPORTING PROCESS, BY TO THE NASCENT POLYPEPTIDE VIA A SIGNAL SEQUENCE, MAINTAINI A STABLE AND PRE-TRANSLOCATION COMPORMATION (BY SIMILARITY)

-I- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                                                                 PROTEIN TRANSPORT; TRANSLOCATION.
SEQUENCE 169 AA; 19132 MW; 74BB8A0E CRC32;
                                                                                                                                                                                                                                                 EMBL; U32758; G1573750; -. TIGR; H10743; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEC
01-NOV-1995 (REL. 32, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P44853;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECB OR HI0743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLEISCHMANN R.D., ADAMS M.D.,
KERLAVAGE A.R., BULT C.J., TOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-EXPORT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
     245 SLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLLAYS-GLIGTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 CQPESRSVSNCLKENYAD-CL-LA-YSGLIGTVMTPN-YV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 CLWQVHAIGGCFWEEFTDLGLQLSNFSAFVNSCLNPVIYV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AILFFNCHILA-SLRRRGERVPSRCG-GPRD-SKSTALILTLVASFLVCWAPYHFFAFLE 272
                                                74 TLEDSGDVAFICEVKQAGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLV 127
                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMLFCSCRDIACTERRRQTIVPV-CSYEERERPNCLSLQDSCKTNY-ICRSRLADF-FTN 266
                                                                                                     14;
                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 25.0%;
25; Conservative
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272
291
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                                                                                                     Conservative
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                                                                                                                         2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%;
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥;
                                                                                                                         Score 95; DB 1;
Pred. No. 1.86e-01
                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99; DB 1;
Pred. No. 4.11e-02
35; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHITE O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                   23;
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                                                                                                                                                   Length 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                 & SECY) THAT
                                                                                                                                                                                                                                                                                                                                                                                                    MAINTAINING
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                                                                                                   1:
     297
                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local S
Matches 1
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13-AUG-1987
01-FEB-1994
01-FEB-1994
                                                                                                                                                                                                                                            P32592;
01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1997 (REL. 35, LAST ANNOTATION UPDATE)
CELL SURFACE ADHESION GLYCOPROTEINS LFA-1, CR3 AND P150,95,
SUBUNIT PRECURSOR (INTEGRIN BETA-2) (CD18 ANTIGEN).
ITGB2 OR CD18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSEMBLY DUDDING, MATURATION, AND INFECTION STACES OF THE VIRAL ASSEMBLY, BUDDING, MATURATION, AND INFECTION STACES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

EMBL; K03456; G328021; -.

EMBL; X04415; G60229; -.

EMBL; X04415; G60229; -.

EMBL; X04415; GAGSMAL.

ATOS. GORE DECEMBLY DOUBLESTERN AVEIGNMENT ATTOM. PROGRESSION.
MEDLINE; 93028437.

SHUSTER D.E., KEHRLI M.E. JR., ACKERMANN M.R., GILBERT R.O.;

PROC. NATL. ACAD. SCI. U.S.A. 89:9225-9229(1992).

-I- FUNCTION: ASSOCIATES WITH ALPHA-L (LFA-1) TO INTERACT WITH ICAM-1,
AND WITH ALPHA-M (MAC-1) OR ALPHA-X TO FORM THE RECEPTOR FOR THE
IC3B FRAGMENT OF THE THIRD COMPLEMENT.

-I- SUBUNIT: DIMER OF AN ALPHA AND BETA SUBUNIT. BETA-2 ASSOCIATES
                                                                                                                                                                                                                  BOS TAURUS (BOVINE).

RETAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS;
                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 92290287.
SHUSTER D.E., BOSWORTH
GENE 114:267-271(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 86245056.
ALIZON M., WAIN-HOBSON S.,
CELL 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE) (H
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND;
                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHO
EUTHERIA; ARTIODACTYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                     WARIANT LAD GLY-128.
MEDLINE; 93028437.
                                                                                                                                                                                                                                                                                                                                                         ITB2_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 18; Consen
                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                             27
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                                                                                                                                                                                                                                                                                                                                                                                                                              KYR-LKHLVWASRELERFALNPGLLETGEGCQQIMEQL-QSTL 67
                                                                                                                                                                                                                                                                                                                                                                                                                  KYRTLRQCV-AGKETN-FSLTSGL-EAKDECRSAMEALKQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORE PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%;
larity 41.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L. 05, CREATED)
L. 28, LAST SEQUENCE UPDATE)
L. 28, LAST ANNOTATION UPDATE)
(CONTAINS: CORE PROTEINS P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN; POLYPROTEIN; MYRISTYLATION; PHOSPHORYLATION.

0 BY SIMILARITY.
1 MYRISTATE (BY SIMILARITY).
137 CORE PROTEIN P17 (MATRIX PROTEIN).
368 CORE PROTEIN P24 (CORE ANTIGEN).
383 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN P7 (NUCLEOCAPSID PROTEIN P1.
437 CORE PROTEIN P1.
453 CORE PROTEIN P1.
504 CORE PROTEIN P6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56001
                                                                                                                                                B.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONTAGNIER L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 1; I
Pred. No. 1.28e-01;
11; Mismatches 9
                                                                                                                                                KEHRLI M.E. JR.;
                                                                                                                                                                                                                        VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4500CD44 CRC32;
                                                                                                                                                                                                                                                                                                                                                         769
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                                                                                                                                                                                                                        TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SONIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NUCLEOCAPSID PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P7,
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Best Local
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CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
REPEAT
REPEAT
                                                                                                                                               MS2_MOUSE STANDARD; PRT; 826 AA. (005910; 01-NOV-1995 (REL. 32, CREATED) 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) CELL SURFACE ANTIGEN MS2 PRECURSOR (EC 3.4.24.-) RICH GLYCOPROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                               ADAM8 OR MS2.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷
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PRELIMINARY STRAIN-ICR;
                                 AKIZUKI S.
SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                       YAMAMOTO
                                                                    STRAIN-ICR;
                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JC1121; JC1121
                                                                                                                                                                                                                                                                                       528 KIYGQ-FCECDNVNC-ER
                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                          477 IGKNCECQTQGRSSQELEGSCRKDNSS-II-CS-GLGDCICGQCVCHTS----D-VPNK 527
                                                                                                                                                                                                                                                                  207 HSYGMLFCSCRDIACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BONDS.

BONDS.

DISEASE: DEFECTS IN CD18 ARE THE CAUSE OF LEUKOCYTE ADHESION DISEASE: DEFECTS IN CD18 ARE THE CAUSING LAD (GLY-128) IS PREVALENT AMONG HOLSTEIN CAUTLE THROUGHOUT THE WORLD, PLACING THIS DISORDER AMONG THE MOST COMMON GENETIC DISEASES KNOWN IN ANIMAL AGRICULTURE. ALL CATTLE WITH THE MUTANT ALLELE ARE RELATED TO ONE BULL, WHO THROUGH THE USE OF ARTIFICIAL INSEMINATION SIRED MANY CALVES IN THE 1950S AND 1960S.

- SIMILARATY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF SIMILARATY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF CELL-SURFACE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WITH DIFFERENT ALPHA CHAINS.
SUBCELLULAR LOCATION: TYPE I MI
PTM: THE CYSTEINE RESIDUES ARE
                                                                                                                                                                                                                                                                                                              ISKGNNCLDAAKAC-NLDDTCKKYRSAYITPCTTSMSNEVCNRRKCHKALRQFFDKVPAK 206
                                                                                                                                                                                                                                                                                                                                                                      1 2.8%;
Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00243;
PS00022;
PS01186;
                                                       s:
                                                                                                    RODENTIA.
                                 (JAN-1996)
           SEQUENCE FROM
                                                        YOSHIYAMA
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; INTEGRIN_BETA; 3.
22; EGF_1; UNKNOWN_2.
86; EGF_2; UNKNOWN_2.
ADHESION; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
MATRIX; CYTOSKELETON; SIGNAL; DISEASE MUTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                    769
617
540
581
581
501
116
501
128
                                                                                                                CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                          84400
                                  TO EMBL/GENBANK/DDBJ DATA BANKS
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                                                                                                                                                                                                                                                                                        543
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                                                       SETOGUCHI M.,
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Pred.
20; M
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POTENTIAL.
POTENTIAL.
POTENTIAL.
O -> G (IN LAD).
46F481EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
INTEGRIN BETA-2.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I MEMBRANE PROTEIN.
ARE INVOLVED IN INTRACHAIN DISULFIDE
                                                                                                                                                                                                                                                                                                                                                          re 96; DB 1; Len
d. No. 1.28e-01;
Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACHMENT SITE (POTENTIAL).
                                                        MATSUURA K.,
                                                                                                                 TETRAPODA; MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEATS
                                                                                                                                                                                                                                                                                                                                                                                 Length 769
                                                                                                                                                              (MACROPHAGE CYSTEINE-
                                                                                                                                                                                                                                                                                                                                                           Indels 12;
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: Tue Jun 23 18:29:33 1998 Job time: 51 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X MEDLINE; 91197896.

A YOSHIDA S., SETOGUCHI M., HIGUCHI Y., AKIZUKI S., YAMAMOTO S.;

INT. IMMUNOL. 2:585-591(1990).

C -!- FUNCTION: POSSIBLE INVOLVEMENT IN EXTRAVASATION OF LEUKOCYTES.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SINGLARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.

REMBL; X13335; E254744; -.

REMBL; X13335; E254744; -.

REMBL; X13335; E254744; -.

REMBL; X13335; E254744; -.

REMBL; X1335; E254744; -.

REMBL; X135; E254744; -.

REMBL; X135; E254744; -.

REMBL; X135; E254744; -.

REMBL; X135
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.8%;
Best Local Similarity 31.4%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
METAL
ACT_SITE
METAL
METAL
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE; GLYCOPROTEIN; ANTIGEN; ZINC; HYDROLASE;
METALLOPROTEASE; SIGNAL.
                                                                                                                                                                                                       90046 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

CYTOPLASMIC (POTENTIAL).

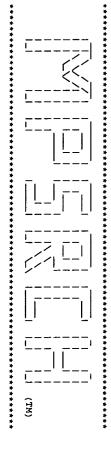
ZINC (CATALYTIC) (PROBABLE).

BY SIMILARITY.

ZINC (CATALYTIC) (PROBABLE).

ZINC (CATALYTIC) (PROBABLE).

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 96; DB 1; Length 826;
Pred. No. 1.28e-01;
12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
7C26F36F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL SURFACE ANTIGEN MS2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          9
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: bular output not generated. Tue Jun 23 18:29:51 1998; MasPar time 28.43 Seconds 693.273 Million cell updates/sec

Title:

Description: Perfect Score: Sequence: >US-08-866-354-4
(1-48) from US08866354.pep
3384
1 MFLATLYFALPLLDLLMSAE.....PVLMLTALAALLSVSLAETS 468

Scoring table: PAM 150 Gap 11

Searched:

140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mbc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 46.587; Variance 79.510; scale 0.586

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11 P89796 (2.9 130 11 036772 MA-P17	3.0 492 11 Q80624 GAG	3.0 486 11 Q77804 GAG	9 Q50790 C	3.0 262 9 Q50381 E	3.0 133 11 Q97725 MATRIX	3.0 130 11 036808 MA-P17 (. 100 3.0 130 11 036786 MA-P17	3.0 129 11 Q97845 MATRIX	20.6 397 10 035325 G	20.6 397 10 035118	46.0 464 2 O15328 I	46.0 464 2 015316 (46.2 464 10 035977 (91.3 460 2 015507 RET	96.0 463 10 035252 GDNF	10 035748	98.7 468 10 035246 GDNF	Result Query No. Score Match Length DB ID Descript:
	*	0624 GAG PROTEIN.	0	0790 ORIGIN OF REPLICATION	0381 DNAN PROTEIN (FRAGMENT		7	7	7	5325 GLIAL CELL LINE-DERIVE	5118 GFRALPHA-3.	_	5316 GLIAL CELL LINE-DERIVE	GLIAL CELL	_		5748 GDNFR-ALPHA/TRNR1-DELT		Description
3.57e-01	4.95e-01	9.44e-02	2.57e-01	9.44e-02	1.85e-01	2.57e-01	2.57e-01	2.57e-01	2.57e-01	4.86e-131	4.86e-131	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.

4 4 5	43	42	41	40	39	38	37	36	35	34	<u>3</u> 3	32	31	30	29	28	27	26	25	24	23	22	21
95 95	96	96	95	96	95	95	95	95	95	95	95	95	95	95	95	96	96	96	96	95	96	97	98
	2.8							•											•		•		•
492 1 623	492 11					130 1					130 1					130 11		130 11		129 11	70 1	1217	1127
1 Q74452 8 Q39204	_		_	_		_		1 075883					_		_	•	•	Q7694			1 P89780	9 045440	3 Q94248
GAG POLYPROTEIN. BHLH PROTEIN.			GAG PROTEIN.	MATRIX PROTEIN P17 (FR	GAG PROTEIN (FRAGMENT)	_	GAG PROTEIN (FRAGMENT)	GAG PROTEIN (FRAGMENT)	MA-P17 (FRAGMENT).	MA-P17 (FRAGMENT).	GAG PROTEIN (FRAGMENT)	MNXG.	CODED FOR BY C. ELEGAN										
1.30e+00 1.30e+00	9.44e-01	9.44e-01	1.30e+00	9.44e-01	1.30e+00	9.44e-01			•		9.44e-01	6.85e-01	4.95e-01										

ALIGNMENTS

Qy	В	Qy	В	Qy	В	Qγ	B	ž A O	SQ	DR	2	RA	ਨ :	7 Z	RL	RΑ	ਨ	RP !	Z (38	20	G N	DE	ij	ij ;	3 ?	SE	RESULT
181 SMSNEVCNRRKCHKALROFFDKVPAKHSYGMLFCSCRDIACTERRROTIVPVCSYEERER 240	181 SMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDVACTERRRQTIVPVCSYEERER 240	121 YEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTT 180	121 YEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTT 180	61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYQSLQGNDLLEDSP 120	61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRGMKKEKNCLRIYWSMYOSLOGNDLLEDSP 120	1 MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60	1 MFLATLYFYLPLLDLLMSAEVSGGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60	Query Match 98.7%; Score 3341; DB 10; Length 468; Best Local Similarity 97.6%; Pred. No. 0.00e+00; Matches 457; Conservative 10; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 468 AA; 51752 MW; AFDCE6A1 CRC32;		SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	DEY B.K. WONG Y.W. TOO H.P.:	STRAIN-C57: TISSUE-LIVER:	CEOTIENCE FROM N A	NEUROREPORT 9:0-0(0001).	DEY B.K., WONG Y.W., TOO H.P.;	STRAIN=C57; TISSUE=LIVER;	SEQUENCE FROM N.A.	[1]	EURARYOTA; METAZOA; CHOKDATA; VEKTEBRATA; TETRAPODA; MAMMADIA;	MUS MUSCULUS (MOUSE).	GDNFR-ALPHA.	GDNF RECEPTOR ALPHA.	(TREMBLREL. 05, LAST	01-JAN-1998 (TREMBLEEL, 05, LAST SEQUENCE UPDATE)	TOPMOTORT.	O35246 PRELIMINARY; PRT; 468 AA.	1

PRT;

463

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Best Loc
Matches
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035748;
01-JAN-1998
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDAT)
GDNER-ALPHA/TRNR1-DELTA PROTEIN.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPOI
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHONG J., ANNIES M., HEUMANN R.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; AJ002072; E1154274; -.
SEQUENCE 463 AA; 51032 MW; 93277F91 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-HANNOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                    416
                                                                          361
                                                                                                356
                                                                                                                      301
                                                                                                                                           296
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YEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITPCTT
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                                           GKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS 463
                                                                                      | OTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDF
                                                                                                                                 YVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPV
                                                                                                                                                               GKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS
                                                                          QTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDF
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llarity 98.9%;
Conservative
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Pred. No. 0.00e+00;
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Best Local S
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O1-JAN-1998 (TREMBLREL.
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                                        RET LIGAND
RETL1.
                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                             DEY B.K., WONG Y.W., TOO H.P. SUBMITTED (JUL-1997) TO EMBL/C EMBL; AF015172; G2624953; -SEQUENCE 463 AA; 51134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNFR-BETA.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
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SEQUENCE FROM
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larity 96.6%;
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TO EMBL/GENBANK/DDBJ DATA
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LAST ANNOTATION
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Pred. No. 0.00e+00;
10; Mismatches 1
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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O35977;

O35977;

O1-JAN-1998 (TREMBLREL. 0)

GLIAL CELL LINE-DERIVED NI
GLIAL CELL LINE-D
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SUBMITTED (OCT-1997) TO EMBL/ CEMBL; U97144; G2282026; -.

EMBL; U97847; G2459742; -.

EMBL; U97847; G2459742; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WALUS L., ROBINSON S.,
PEPINSKY R.B., CATE R.I.
PEPINSKY R.B., CATE R.I.
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SANICOLA M., HESSION C.A.,
    SEQUENCE FROM N.A
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SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA
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larity 91.8%;
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                                                              CHORDATA;
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. 05, LAST SEQUENCE UPI
. 05, LAST ANNOTATION UPI
D NEUROTROPHIC FACTOR F
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JAWORSKI G.,
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Pred. No. 0.
27; Mismatc
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H., TIZARD R.,
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SANICOLA M., HESSION C.
WALUS L., ROBINSON S.,
PEPINSKY R.B., CATE R.L
                                                       SEQUENCE FROM N.A.
TISSUE-FETAL BRAIN;
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SANICOLA M., HESSION
  WARTIOVAARA K., SUVANTO P.,
MOSHNYAKOV M., AIRAKSINEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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JAWORSKI G
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EMBL/GENBANK/DDBJ
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Pred. No. 0.00e+00;
  HORELLI-KUITUNEN
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        SAARMA M.;
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                                                            SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R. PEPINSKY R.B., CATE R.L., SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL, U97145; G2282028; -
                                                                                                                                                                 SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZAR PEPINSKY R.B., CATE R.L., PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
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                                                                                                                                                                                                                                                                  RETL2.
HOMO SAPIENS (HUMAN).
------ METAZOA; CHORDATA;
                                                                                                                             TISSUE-LIVER;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                     TISSUE-LIVER;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            EUTHERIA; PRIMATES.
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Local Similarity 48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  E--LTTNIIPGSNKVIKPNSGPSRARPSAALTVLSVLMLKQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPVQTTTATTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLS
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  . Similarity
224; Conser
  Conservative
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             46.0%; Score 1556; DB 2;
48.4%; Pred. No. 0.00e+00;
                                                   51543
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 101;
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101; Mismatches 120; Indels 18;
                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                   288A8BD8
  Mismatches
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                         Length 464;
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Best Local Similarity
Matches 120; Conser
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035118; PRELIMINARY;
035118; PREMBLREL. 05, C
01-JAN-1998 (TREMBLREL. 05, L
01-JAN-1998 (TREMBLREL. 05, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL6; TISSUE-HEART;
NOMOTO S., ITO S., YANG L., ADACHI K., KIU
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ
EMBL; AB00883; D1024441; -.
SEQUENCE 397 AA; 44307 MW; A80E0D24 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
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                                                                                                                                                  DSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTCKKYRSAYITP
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PS-VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDI-LGTCATEQ-SRCLRAYLGLIGT
                                                                                               CS-GIR----CORHICLAQUESFFEKAAESHAQGLILCPCAPEDAGCGERRRNTIAPSCAL
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                                               CTTSMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC-R-DIACTERRRQTIVPVCSY
                                                                                                                                                                                                                                                                                    GPSFQATQAPRV-E-KTPSLPDDLSDSTS-LGTSVITTCTSVQEQGLKANNSKELSMCFT
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llarity 34.4%;
Conservative
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 696; DB 10; I
Pred. No. 4.86e-131;
71; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
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Best Local S
Matches 12
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035325
035325;
01-JAN-1998 (TREMBLREL 0
                                                                                                                                                                                                                                                                                                                                                                                                     Q97845;
Q1-FEB-1997
Q1-FEB-1997
Q1-FEB-1997
STRAIN-BAB MNT;
MARWA R., ROQUES P., COURPOTIN C.,
ROANE A., MARC D., LASFARGUES G., I
J. VIROL. 70:4474-4483(1996).
EMBL; X99948; E258593; -.
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TRUPP M., RAYNOSCHEK C., IBANEZ C.F.;
SUBMITITED (SEP-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF020305; G2429367; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFRA-3.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
VIRIDAE; SS-RNA ENVELOPED VIRUSES; 1
LENTIVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q97845
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                                                                                                                                                                     SEQUENCE FROM N.A.
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Local Similarity 34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMTPNYVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMTPNYVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQA
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                                                                                                                                                                                                                                                                                                                                                                   7 (TREMBLREL. 02, CRE
7 (TREMBLREL. 02, LAS
7 (TREMBLREL. 02, LAS
TEIN P17 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 AA; 44333 MW; F0C0C841 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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05, LAST SEQUING OS, LAST ANNO NEUROTROPHIC
                                                                                                                                                                                                                                                                                                                                                                                                     02, CREATED)
02, LAST SEQUENCE UPDATE)
02, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 696; DB 10; 1
Pred. No. 4.86e-131;
71; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                       PARNETMATHIEU
                                                                                                                                                                                                                                                                      l (HIV-1).
POSITIVE-STRAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129
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                                                                                                       BOUSSIN
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RESULTA
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                                       Query Match
Best Local S
Matches 1
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Best Local Similarity 41.9%;
Matches 18; Conservative
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Best Local :
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036786;
01-JAN-1998
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O36808;
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O1-JAN-1998
O1-JAN-1998
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                 HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1). VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
LEIGH BROWN A.J., LOBIDEL D., WADE C.M., REBUS S
BRETTLE R.P., FRANCE A.J., LEEN C.S., MCMENAMIN
MAW R.D., MULCAHY F., ROBERTSON J.R., SANKAR K.N
PEUTHERER J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATRIX PROTEIN NON_TER 129
                                                                                                                             SEQUENCE
                                                                                                                                                                                        VIROLOGY 235:166-177(1997).
EMBL; AF014205; G2406752; -.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

LEIGH BROWN A.J., LOBIDEL D., WADE C.M., REBUS S., PHILLIPS N

BRETTLE R.P., FRANCE A.J., LEEN C.S., MCMENAMIN J., MCMILLAN

MAW R.D., MULCAHY F., ROBERTSON J.R., SANKAR K.N., SCOTT G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MA-P17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIROLOGY 235:166-177(1997).
EMBL; AF014183; G2406708; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA-P17 (FRAGMENT).
                                                                                                                                                                                                                                    PEUTHERER J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENTIVIRINAE
                                                                                                                                                                                                                                                                                                                                                               LENTIVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.0%;
Local Similarity 41.9%;
les 18; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
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  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KYK-LKHIVWASRELERFAVNPGLLETSEGCRQIMEQL-QPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYRTLRQCV-AGKETN-FSLTSGL-EAKDECRSAMEALKQKSL
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KYK-LKHIVWASRELERFAVNPGLLETSEGCRQIMEQL-QSAL
                                                             3.0%;
Similarity 39.5%;
                                                                                                                           130
130 AA;
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130 AA;
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8 (TREMBLREL. 05,
8 (TREMBLREL. 05,
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                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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14550 MW;
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14584 MW;
                                                                                                                           14527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95,05
                                     Score 100; DB 11; 1
Pred. No. 2.57e-01;
12; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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Pred. No. 2.57e-01;
11; Mismatches 9
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Pred. No. 2.57e-01;
11; Mismatches 9
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LAST ANNOTATION UPDATE)
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                                                                                                                             7325723C CRC32;
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                                                                                 Length
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                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RETROVIRIDAE;
                                                                                   130;
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Best Local (
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050790
050790;
050790;
01-NOV-1996
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               050381; PRELIMINARY; PRT; 262 AA.
050381; O1-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 13
Q97725
Q97725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 96062237.
RAJACOPALAN M. OIN M.H., NASH D.R.,
J. BACTERIOL. 177:6527-6535(1995).
EMBL: U17833; 61079500; -.
RON_TER 262 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATRIX PROTEIN.
NON_TER 133
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ROANE A., MARC D., LASFARGUES G., J
J. VIROL. 70:4474-4483(1996).
EMBL; Z79562; E261908; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
01-FEB-1997 (TREMBLREL.)
MATRIX PROTEIN P17 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=2-MC155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCOBACTERIUM SMEGMATIS. PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PAL-M;
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VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENTIVIRINAE.
                                                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                   172 ESVVLAATDRERLAVRELTWYTTAGDVEAAVLVPAKTL-AEAAKAGTDGNQVHLALGSGA 230
                                                                                                                                                                                                                                                                           231 SVGKDGLLGIRS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 3.0%;
Local Similarity 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 KYRTLRQCV-AGKETN-FSLTSGL-EAKDECRSAMEALKQKSL 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 3.0%;
Local Similarity 44.2%;
es 19; Conservative
                                                                                                                                                                                                                        DFGKDGLAGASS
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262 AA; 27269 MW;
(TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 11; I
Pred. No. 2.57e-01;
9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 9;
Pred. No. 1.85e-01;
14; Mismatches 33
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 33;
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                                                                                                          399 AA.
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                                                                                                              Query Match 3.0%;
Best Local Similarity 27.7%;
Matches 28; Conservative
                                                                                                                                                                    SALAZAR L., FSIHI H., DE ROSSI
COLE S.T., TARIFF H.E.;
MICROBIOLOGY 20:283-293(1996).
EMBL; X92504; E208997; -
SEQUENCE 399 AA; 41773 MW;
                                                                                                                                                                                                                                                                                         MYCOBACTERIUM TUBERCULOSIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES;
                                                                                                                                                                                                                                                STRAIN-H37RV;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        DNAN
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                                                                                                                                                                                                                                                                                                                                                 ORIGIN OF REPLICATION AND GENES RNPA, RPMH, DNAA,
                                                                        178 ATDSRLAVRELEWSASSPDIEAAVLVPAKTL-AEAAKAGIGGSDVRLSLGTGPGVGKDGL 236
 426 AGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAE
                                                         368 TTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGS-THLCL-SDSDFGKDGL 425
                            237 LGISGN-GKRSTTRLLDAEFPKFRQLLPTEHTAVATMDVAE 276
                                                                                                                                                                                                                                 DE ROSSI
                                                                                                              Score 103; DB 9;
Pred. No. 9.44e-02;
27; Mismatches 42
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                                                                                                                                                                                                                                 RICCARDI G.,
                                                                                                                                                                          CRC32;
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   466
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